

SEQUENCE LISTING

<110> Kilian, Andrzej

<120> VERTEBRATE TELOMERASE GENES AND PROTEINS AND USES THEREOF

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<140> 09/502,424 <141> 2000-02-11

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Ile Asp His Cys Ile Ile Tyr Leu Leu Thr Gly Glu Leu Tyr Asn Asn 65 70 75 80

Val Leu Thr Phe Gly Tyr Lys Ile Ala Arg Asn Glu Asp Val Asn Asn 85 90 95

Ser Leu Phe Cys His Ser Ala Asn Val Asn Val Thr Leu Leu Lys Gly 100 Ala Ala Trp Lys Met Phe His Ser Leu Val Gly Thr Tyr Ala Phe Val 120 Asp Leu Leu Ile Asn Tyr Thr Val Ile Gln Phe Asn Gly Gln Phe Phe Thr Gln Ile Val Gly Asn Arg Cys Asn Glu Pro His Leu Pro Pro Lys 155 Trp Val Gln Arg Ser Ser Ser Ser Ala Thr Ala Ala Gln Ile Lys 170 Gln Leu Thr Glu Pro Val Thr Asn Lys Gln Phe Leu His Lys Leu Asn 185 Ile Asn Ser Ser Ser Phe Phe Pro Tyr Ser Lys Ile Leu Pro Ser Ser 195 Ser Ser Ile Lys Lys Leu Thr Asp Leu Arg Glu Ala Ile Phe Pro Thr Asn Leu Val Lys Ile Pro Gln Arg Leu Lys Val Arg Ile Asn Leu Thr 230 Leu Gln Lys Leu Leu Lys Arg His Lys Arg Leu Asn Tyr Val Ser Ile 250 Leu Asn Ser Ile Cys Pro Pro Leu Glu Gly Thr Val Leu Asp Leu Ser 265 His Leu Ser Arg Gln Ser Pro Lys Glu Arg Val Leu Lys Phe Ile Ile 275 280 Val Ile Leu Gln Lys Leu Leu Pro Gln Glu Met Phe Gly Ser Lys 295 Asn Lys Gly Lys Ile Ile Lys Asn Leu Asn Leu Leu Leu Ser Leu Pro 305 Leu Asn Gly Tyr Leu Pro Phe Asp Ser Leu Leu Lys Lys Leu Arg Leu 325 330 Lys Asp Phe Arg Trp Leu Phe Ile Ser Asp Ile Trp Phe Thr Lys His Asn Phe Glu Asn Leu Asn Gln Leu Ala Ile Cys Phe Ile Ser Trp Leu Phe Arg Gln Leu Ile Pro Lys Ile Ile Gln Thr Phe Phe Tyr Cys Thr 370 375 380 Glu Ile Ser Ser Thr Val Thr Ile Val Tyr Phe Arg His Asp Thr Trp 390 395

Asn Lys Leu Ile Thr Pro Phe Ile Val Glu Tyr Phe Lys Thr Tyr Leu

405 410 415 Val Glu Asn Asn Val Cys Arg Asn His Asn Ser Tyr Thr Leu Ser Asn Phe Asn His Ser Lys Met Arg Ile Ile Pro Lys Lys Ser Asn Asn Glu 440 Phe Arg Ile Ile Ala Ile Pro Cys Arg Gly Ala Asp Glu Glu Phe 450 455 Thr Ile Tyr Lys Glu Asn His Lys Asn Ala Ile Gln Pro Thr Gln Lys Ile Leu Glu Tyr Leu Arg Asn Lys Arg Pro Thr Ser Phe Thr Lys Ile 490 Tyr Ser Pro Thr Gln Ile Ala Asp Arg Ile Lys Glu Phe Lys Gln Arg 505 Leu Leu Lys Lys Phe Asn Asn Val Leu Pro Glu Leu Tyr Phe Met Lys 520 Phe Asp Val Lys Ser Cys Tyr Asp Ser Ile Pro Arg Met Glu Cys Met 535 Arg Ile Leu Lys Asp Ala Leu Lys Asn Glu Asn Gly Phe Phe Val Arg 550 555 Ser Gln Tyr Phe Phe Asn Thr Asn Thr Gly Val Leu Lys Leu Phe Asn 565 Val Val Asn Ala Ser Arg Val Pro Lys Pro Tyr Glu Leu Tyr Ile Asp 585 Asn Val Arg Thr Val His Leu Ser Asn Gln Asp Val Ile Asn Val Val Glu Met Glu Ile Phe Lys Thr Ala Leu Trp Val Glu Asp Lys Cys Tyr

Ile Arg Glu Asp Gly Leu Phe Gln Gly Ser Ser Leu Ser Ala Pro Ile

Val Asp Leu Val Tyr Asp Asp Leu Leu Glu Phe Tyr Ser Glu Phe Lys 650

Ala Ser Pro Ser Gln Asp Thr Leu Ile Leu Lys Leu Ala Asp Asp Phe 660 665

Leu Ile Ile Ser Thr Asp Gln Gln Gln Val Ile Asn Ile Lys Lys Leu

Ala Met Gly Gly Phe Gln Lys Tyr Asn Ala Lys Ala Asn Arg Asp Lys 695

Ile Leu Ala Val Ser Ser Gln Ser Asp Asp Asp Thr Val Ile Gln Phe 705 710 715

```
Cys Ala Met His Ile Phe Val Lys Glu Leu Glu Val Trp Lys His Ser
Ser Thr Met Asn Asn Phe His Ile Arg Ser Lys Ser Ser Lys Gly Ile
                                 745
Phe Arg Ser Leu Ile Ala Leu Phe Asn Thr Arg Ile Ser Tyr Lys Thr
                             760
Ile Asp Thr Asn Leu Asn Ser Thr Asn Thr Val Leu Met Gln Ile Asp
    770
                        775
His Val Val Lys Asn Ile Ser Glu Cys Tyr Lys Ser Ala Phe Lys Asp
Leu Ser Ile Asn Val Thr Gln Asn Met Gln Phe His Ser Phe Leu Gln
                805
                                    810
Arg Ile Ile Glu Met Thr Val Ser Gly Cys Pro Ile Thr Lys Cys Asp
Pro Leu Ile Glu Tyr Glu Val Arg Phe Thr Ile Leu Asn Gly Phe Leu
                            840
Glu Ser Leu Ser Ser Asn Thr Ser Lys Phe Lys Asp Asn Ile Ile Leu
    850
                        855
Leu Arg Lys Glu Ile Gln His Leu Gln Ala Tyr Ile Tyr Ile
                    870
His Ile Val Asn
<210> 6
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<212> DNA
<213> Homo sapiens
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<221> intron
<222> (8)..(13)
<223> First six bases of Y intron
<400> 6
ccaggtgggc ctc
                                                                   13
<210> 7
<211> 14
<212> DNA
<213> Homo sapiens
<220>
<221> intron
<222> (1)..(7)
```

<223> Last seven bases of intron Y

<400> 7 gcaggtgtcc tgcc	14
<210> 8	
<211> 14	
<212> DNA	
<213> Homo sapiens	
<220>	
<221> intron	
<222> (8) (14)	
<223> First 7 bases of Intron 1	
<400> 8	
aaagagggtg gctg	14
	14
<210> 9	
<211> 14	
<212> DNA <213> Homo sapiens	
(213) Homo Sapiens	
<220>	
<221> intron	
<222> (1)(7)	
<223> Last 7 bases of Intron 1	
<400> 9	
aacagaagcc gagc	14
<210> 10	
<211> 14	
<212> DNA	
<213> Homo sapiens	
<220>	
<221> intron	
<222> (8)(14)	
<223> First 7 bases of Intron Alpha	
<400> 10	
tgtcaaggtg gatg	14
<210> 11	
<211> 14	
<212> DNA	
<213> Homo sapiens	
<220>	
<221> intron	
<222> (1)(7)	
<223> Last 7 bases of Intron Alpha	
<400> 11	
ccccaggac aggc	14
<210> 12	
<211> 14	
<212> DNA	

```
<213> Homo sapiens
  <220>
  <221> intron
  <222> (8)..(14)
  <223> First 7 bases of Intron Beta
  <400> 12
 gagccacgtc tcta
                                                                       14
 <210> 13
 <211> 14
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> intron
 <222> (1)..(7)
 <223> Last 7 bases of Intron Beta
 <400> 13
 ggggcaagtc ctac
                                                                      14
 <210> 14
 <211> 14
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> intron
 <222> (8)..(14)
 <223> First 7 base of Intron 2
 <400> 14
actccaggtg agcg
                                                                      14
<210> 15
<211> 14
<212> DNA
<213> Homo sapiens
<220>
<221> modified_base
<222> (1)..(7)
<223> Wherein N is any nucleotide
<220>
<221> intron
<222> (1)..(7)
<223> Last 7 bases of Intron 2
<400> 15
nnnnnncta tgcc
                                                                     14
<210> 16
<211> 173
<212> DNA
<213> Homo sapiens
```

```
<220>
  <221> intron
  <222> (8)..(166)
  <223> Full Sequence of Intron 3
  <400> 16
  aacgcagccg aagaaaacat ttctgtcgtg actcctgcgg tgcttgggtc gggacagcca 60
  gagatggagc caccccgcag accgtcgggt gtgggcagct ttccggtgtc tcctgggagg 120
  ggagttgggc tgggcctgtg actcctcagc ctctgttttc ccccagggat gtc
  <210> 17
  <211> 46
  <212> PRT
  <213> Homo sapiens
  <400> 17
 Thr Ala Ala Glu Glu Asn Ile Leu Val Val Thr Pro Ala Val Leu Gly
 Ser Gly Gln Pro Glu Met Glu Pro Pro Arg Arg Pro Ser Gly Val Gly
                                   25
 Ser Phe Pro Val Ser Pro Gly Arg Gly Val Gly Leu Gly Leu
 <210> 18
 <211> 104
 <212> DNA
 <213> Homo sapiens
 <220>
 <223> Intron Y
 <400> 18
ggcctccccg gggtcggcgt ccggctgggg ttgagggcgg ccggggggaa ccagcgacat 60
gcggagagca gcgcaggcga ctcagggcgc ttcccccgca ggtg
<210> 19
<211> 34
<212> PRT
<213> Homo sapiens
<223> Reding Frame One of Intron Y
<400> 19
Gly Leu Pro Gly Val Gly Val Arg Leu Gly Leu Arg Ala Ala Gly Gly
Asn Gln Arg His Ala Glu Ser Ser Ala Gly Asp Ser Gly Arg Phe Pro
             20
                                 25
```

Arg Arg

```
<210> 20
  <211> 10
  <212> PRT
  <213> Homo sapiens
 <223> Reading Frame Two of Intron Y before termination
       Codon
 <400> 20
 Ala Ser Pro Gly Ser Ala Ser Gly Trp Gly
 <210> 21
 <211> 23
 <212> PRT
 <213> Homo sapiens
 <220>
 <223> Reading Frame Two of Intron Y after termination
       Codon
 <400> 21
 Gly Arg Pro Gly Gly Thr Ser Asp Met Arg Arg Ala Ala Gln Ala Thr
                   5
 Gln Gly Ala Ser Pro Ala Gly
              20
 <210> 22
 <211> 34
 <212> PRT
<213> Homo sapiens
<220>
<223> Reading Frame Three of Intron Y
<400> 22
Pro Pro Arg Gly Arg Pro Ala Gly Val Glu Gly Gly Arg Gly Glu
Pro Ala Thr Cys Gly Glu Gln Arg Arg Leu Arg Ala Leu Pro Pro
Gln Val
<210> 23
<211> 38
<212> DNA
<213> Homo sapiens
<220>
<223> Intron 1
```

```
<400> 23
   gtggctgtgc tttggtttaa cttccttttt aaccagaa
                                                                       38
   <210> 24
   <211> 13
   <212> PRT
   <213> Homo sapiens
  <220>
  <223> Intron 1 Translation
  <400> 24
  Val Ala Val Leu Trp Phe Asn Phe Leu Phe Asn Gln Lys
  <210> 25
  <211> 36
  <212> DNA
  <213> Homo sapiens
  <220>
 <223> Intron Alpha
 <400> 25
 gtggatgtga cgggcgcgta cgacaccatc ccccag
                                                                      36
 <210> 26
 <211> 12
 <212> PRT
 <213> Homo sapiens
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 <223> Intron Alpha Translation
 <400> 26
 Val Asp Val Thr Gly Ala Tyr Asp Thr Ile Pro Gln
                   5
 <210> 27
 <211> 182
<212> DNA
<213> Homo sapiens
<220>
<223> Intron Beta
<400> 27
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accagecege tgagggatge egtegteate gageagaget eeteeetgaa tgaggecage 120
agtggcctct tcgacgtctt cctacgcttc atgtgccacc acgccgtgcg catcaggggc 180
                                                                    182
<210> 28
<211> 61
<212> PRT
<213> Homo sapiens
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```
<220>
   <223> Intron Beta Translation
   <400> 28
   Val Ser Thr Leu Thr Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala
  His Leu Gln Glu Thr Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln
                                    25
  Ser Ser Ser Leu Asn Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu
  Arg Phe Met Cys His His Ala Val Arg Ile Arg Gly Lys
  <210> 29
  <211> 226
  <212> DNA
  <213> Homo sapiens
  <220>
  <223> Intron 2
  <400> 29
 gtgagcgcac ctggccggaa gtggagcctg tgcccggctg gggcaggtgc tgctgcaggg 60
 cegttgegte caectetget teegtgtggg geaggegaet gecaateeea aagggteaga 120
 tgccacaggg tgcccctcgt cccatctggg gctgagcaca aatgcatctt tctgtgggag 180
 tgagggtgcc tcacaacggg agcagttttc tgtgctattt tggtaa
 <210> 30
 <211> 159
 <212> DNA
 <213> Homo sapiens
 <220>
 <223> Intron 3
 <400> 30
 ccgaagaaaa catttctgtc gtgactcctg cggtgcttgg gtcgggacag ccagagatgg 60
 agccaccccg cagaccgtcg ggtgtgggca gctttccggt gtctcctggg aggggagttg 120
ggctgggcct gtgactcctc agcctctgtt ttcccccag
<210> 31
<211> 44
<212> PRT
<213> Homo sapiens
<220>
<223> Intron 3 Translation
<400> 31
Ala Glu Glu Asn Ile Ser Val Val Thr Pro Ala Val Leu Gly Ser Gly
Gln Pro Glu Met Glu Pro Pro Arg Arg Pro Ser Gly Val Gly Ser Phe
```

```
Pro Val Ser Pro Gly Arg Gly Val Gly Leu Gly Leu
                                  40
    <210> 32
    <211> 262
    <212> DNA
    <213> Homo sapiens
    <220>
   <223> Intron X. Complete length unknown
   <400> 32
   gacagtcacc aggggggttg accgccggac tgggcgtccc cagggttgac tataggacca 60
   ggtgtccagg tgccctgcaa gtagaggggc tctcagaggc gtctggctgg catgggtgga 120
   cgtggccccg ggcatggcct tetgcgtgtg etgccgtggg tgccctgagc cetcactgag 180
   teggtggggg ettgtggett eeegtgaget teeecetagt etgttgtetg getgageaag 240
   <210> 33
   <211> 218
  <212> DNA
  <213> Homo sapiens
  <220>
  <223> Partial Sequence of Genomic Intron (approximately
  <400> 33
  gtggctgtgc tttggtttaa cttccttttt aaccagaagt gcgtttgagc cccacatttg 60
 gtatcagett agatgaaggg eeeggaggag gggeeaeggg acaeageeag ggeeatggea 120
 cggcgcccac ccatttgtgc gcacagtgag gtggccgagg tgccggtgcc tccagaaaag 180
 cagcgtgggg gtgtaggggg agctcctggg gcagggac
 <210> 34
 <211> 2031
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> modified_base
 <222> (1767)..(1769)
 <223> Wherein N is A, C, G or \mathtt{T}
<220>
<223> N-Terminal Truncated Telomerase
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gtgctgccgc tggccacgtt cgtgcggcgc ctggggcccc agggctggcg gctggtgcag 120
cgcggggacc cggcggcttt ccgcgcgctg gtggcccagt gcctggtgtg cgtgccctgg 180
gacgcacggc cgcccccgc cgcccctcc ttccgccagg tgtcctgcct gaaggagctg 240
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ttegegetge tggaegggge eegeggggge eeceeegagg eetteaceae eagegtgege 360
agctacetge ccaacaeggt gacegaegea etgeggggga geggggegtg ggggetgetg 420
ctgcgccgcg tgggcgacga cgtgctggtt cacctgctgg cacgctgcgc gctctttgtg 480
```

```
ctggtggctc ccagctgcgc ctaccaggtg tgcgggccgc cgctgtacca gctcggcgct 540
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cgggcctgga accatagcgt cagggaggcc ggggtccccc tgggcctgcc agccccgggt 660
gcgaggaggc gcgggggcag tgccagccga agtctgccgt tgcccaagag gcccaggcgt 720
ggcgctgccc ctgagccgga gcggacgccc gttgggcagg ggtcctgggc ccacccgggc 780
aggacgcgtg gaccgagtga ccgtggtttc tgtgtggtgt cacctgccag acccgccgaa 840
gaagccacct ctttggaggg tgcgctctct ggcacgcgcc actcccaccc atccgtgggc 900
cgccagcacc acgcgggccc cccatccaca tcgcggccac cacgtccctg ggacacgcct 960
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gegeagtgee cetaeggggt geteeteaag acgeaetgee egetgegage tgeggteace 1260
ccagcagecg gtgtctgtgc ccgggagaag ccccaggget ctgtggegge ccccgaggag 1320
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gccaagetet egetgeagga getgaegtgg aagatgageg tgegggaetg egettggetg 1560
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ctggccaagt teetgeactg getgatgagt gtgtacgteg tegagetget caggtettte 1680
ttttatgtca cggagaccac gtttcaaaag aacaggctct ttttctaccg gaagagtgtc 1740
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tgccgtgggt gccctgagcc ctcactgagt cggtggggc ttgtggcttc ccgtgagctt 1980
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<211> 588
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<220>

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His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly

Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg 40

Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro

Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Lys Glu Leu 70

Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val 85

Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro 100 105

Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr

420

DIO

Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Arg Arg Val 135 Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr 170 Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly Pro Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg 215 Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg 230 235 Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp 245 Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val 265 Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala 280 Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly 325 Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser 360 Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln 375 Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His 390 395 Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln

430

```
Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu
         435
 Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe
                         455
Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser
                     470
                                         475
Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser
                                     490
Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met
                                 505
Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys
        515
Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe
                        535
Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe
545
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                                                             560
Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr
Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly
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<213> Homo sapiens
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ggcgctgccc ctgagccgga gcggacgccc gttgggcagg ggtcctgggc ccacccgggc 780
aggacgcgtg gaccgagtga ccgtggtttc tgtgtggtgt cacctgccag acccgccgaa 840
```

DIO

gaagccacct ctttggaggg tgcgctctct ggcacgcgcc actcccaccc atccgtgggc 900 cgccagcacc acgcgggccc cccatccaca tcgcggccac cacgtccctg ggacacgcct 960 tgtccccgg tgtacgccga gaccaagcac ttcctctact cctcaggcga caaggagcag 1020

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 gtggagacca tctttctggg ttccaggccc tggatgccag ggactccccg caggttgccc 1140
 cgcctgcccc agcgctactg gcaaatgcgg cccctgtttc tggagctgct tgggaaccac 1200
 gcgcagtgcc cctacggggt gctcctcaag acgcactgcc cgctgcgagc tgcggtcacc 1260
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 gccaagetet egetgeagga getgaegtgg aagatgageg tgegggaetg egettggetg 1560
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Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Lys Glu Leu
Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val
Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Pro Pro
                                105
Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr
        115
Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val
                        135
Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val
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70

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35

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Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro 690 Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile 710 Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln 730 Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His 745 Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu Thr Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu Thr Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu Asn Glu 790 Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys His His

Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly Ile Pro 825

Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly Asp 840

Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu Leu 855

Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His Ala 865 870

Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly Cys 890

Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp Glu 905

Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly Leu Phe

Pro Trp Cys Gly Leu Leu Asp Thr Arg Thr Leu Glu Val Gln Ser 940

Asp Tyr Ser Arg 945

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<211> 3362

<212> DNA

<213> Homo sapiens

<220>
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Beta and 3

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DIE

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Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg

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	235
230	235 Glu Arg Thr Pro Val Gly Gln Gly Ser Trp 255 250 The Pro Ser Asp Arg Gly Phe Cys Val 270
225	Arg Thr Pro Val Gif 255
nla Pro Glu Pro (Arg Gly Pro Ser Asp Arg Gly Phe Cys Val Arg Gly Pro Ser Asp Arg Gly Phe Cys Val 270 265 201 Glu Ala Thr Ser Leu Glu Gly Ala 285
Gly Ala Ala 245	Ser Asp Arg Gly 270
arg Thr	Arg Gly Pio Son 265
Nia His Pro Gly Alg	Ser Leu Glu Gly Ald
A10 260	Ala Glu Glu Ala Thi 331 285
- Pro Ala Arg Pro	Arg Gly Pro 265 Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala 285 280 Ser His Pro Ser Val Gly Arg Gln His His 300 295 297 Pro Pro Arg Pro Trp Asp Thr Pro 320
Val Ser 275	nro Ser Val Gly Arg
ara Hi	s Ser His Pro
Leu Ser Gly Thr Ars	295 Arg Pro Trp Asp Thi 320
290	295 Arg Pro Trp Asp Thr Pro 320 315 10 Try Lvs His Phe Leu Tyr Ser Ser Gly 335
gly pro pro Ser II	ar Ser Arg Tro 315 315 10 10 11a Glu Thr Lys His Phe Leu Tyr Ser Ser Gly 335 330 330 330 330 330
Ala Giy	The Lys His Phe Leu 191 335
TOT A	la Glu Thi Bro 330
Cys Pro Pro Val 325	Leu Ser Ser Leu Arg
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Lys Glu Gln Leu	Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro 345 Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser 365 360 Arg Arg Leu Pro Arg Leu Pro Gln
Gly Ala	Arg Arg 160 Pro Gln
Ser Leu Thr Gly 1.2	arg Leu Pro Arg Leu II
7.	Gly Thr Pro Arg Arg 380
Arg Pro Trp Met Pic	Arg Arg Leu Var 360 Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln 380 375 380 400
Trp Gln Me	Yr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg 415 410 OS Arg Pro Leu Arg 415 410 Arg Glu Lys Pro Gln 430
Arg Tyr 12F	Leu Lys Thr His Cys 124 415
Ala Gln Cys Plo 2	.05 Arg Glu Lys Plo of
ala Val Thr	yr Gly Val Leu 2410 410 05 Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln 430 425 Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu 445 440 The Ser Pro Trp Gln Val Tyr Gly Phe
Tala	Ala Pro Glu 440
Gly Ser Val 12	pro Trp Gln Val Tyr Gar
val Gln Leu Leu	Ala Pro Glu Glu 440 Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe 460 455 Val Pro Pro Gly Leu Trp Gly Ser 480
~ ∧la CY	s Leu Arg Alg 2
Val Arg Al	Arg Gln His Ser Job 400 455 S Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser 480 470 Arg Asn Thr Lys Lys Phe Ile Ser 495
Arg His Asn G.	485 Clu Leu Thr Trp Lys No
Cly Lys H	Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys Asp Cys Ala Trp Leu Arg Glu Glu Ile Leu Ala Lys Phe
	Asp Cys Ala Trp 1520 520 trg phe
Ser Val Arg	Asp Cys Ala Trp Leu Als 520 Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe 540 535
515	540
pro Ala	Ala Glu ni 535
Val F10	

Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr 570 Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His 585 Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln 600 His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val 630 Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg 660 Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg 680 Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro 695 Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln 730 Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His 745 Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu Thr Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu Thr Ser 770

Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Leu Asn Glu

Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys His His

Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly Ile Pro

Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly Asp

790

805

835

Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu 850 855 860

Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His Ala 865 870 875 880

Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly Cys 885 890 895

Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp Glu 900 905 910

Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly Leu Phe 915 920 925

Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val Gln Ser 930 935 940

Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu Thr Phe 945 950 955 960

Asn Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu Phe Gly 965 970 975

Val Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln Val Asn 980 985 990

Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu Gln 995 1000 1005

Ala Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe His Gln Gln 1010 1015 1020

Val Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp Thr Ala 1025 1030 1035 1040

Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala Glu Glu Glu Asn 1045 1050 1055

Ile Leu Val Val Thr Pro Ala Val Leu Gly Ser Gly Gln Pro Glu Met 1060 1065 1070

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Gly Arg Gly Val Gly Leu Gly Leu 1090 1095

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<213> Homo sapiens

<220>

<223> Protein that lacks Motif A; with Intron Beta

<400> 45

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DIO

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<400> 46
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His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
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Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
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Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Lys Glu Leu
Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val
Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Pro Pro
                                105
Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr
                            120
Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val
                        135
Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val
                    150
                                        155
Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr
                165
Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly
                                185
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205

Pro Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg

200

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Ser Val Arg (Asp tys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys

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Cys Tyr Gly Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His 855 Leu Thr His Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro 875 Glu Tyr Gly Cys Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro 890 Val Glu Asp Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala 905 His Gly Leu Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val Gln Ser Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala 935 Ser Leu Thr Phe Asn Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg 945 950 960 Lys Leu Phe Gly Val Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln Val Asn Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile 985 990 Leu Leu Gln Ala Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro 1000 Phe His Gln Gln Val Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile 1010 1015 Ser Asp Thr Ala Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala 1025 1035 Gly Met Ser Leu Gly Ala Lys Gly Ala Ala Gly Pro Leu Pro Ser Glu 1050 Ala Val Gln Trp Leu Cys His Gln Ala Phe Leu Leu Lys Leu Thr Arg 1060 His Arg Val Thr Tyr Val Pro Leu Leu Gly Ser Leu Arg Thr Ala Gln 1080 1085 Thr Gln Leu Ser Arg Lys Leu Pro Gly Thr Thr Leu Thr Ala Leu Glu 1090 1095

1115

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DIO

215

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Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His 290 295 300

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Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly 325 330 335

Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro 340 345 350

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Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met 500 505 510

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410

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DID

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Lys Ala Ala His Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser 745 Thr Leu Thr Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu 760 Gln Glu Thr Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu Asn Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe 795 Met Cys His His Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly Ile Pro Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu 825 Cys Tyr Gly Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp 835 Gly Leu Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro 870 Glu Tyr Gly Cys Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala 905 His Gly Leu Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val Gln Ser Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu Thr Phe Asn Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu Phe Gly Val Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp 965 970 Leu Gln Val Asn Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile 980 Leu Leu Gln Ala Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro 1000 Phe His Gln Gln Val Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile 1010

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1035

57

Glu Glu Glu Asn Ile Leu Val Val Thr Pro Ala Val Leu Gly Ser Gly 1045 1050 Gln Pro Glu Met Glu Pro Pro Arg Arg Pro Ser Gly Val Gly Ser Phe 1060 1065 Pro Val Ser Pro Gly Arg Gly Val Gly Leu Gly Leu 1080 <210> 51 <211> 2135 <212> DNA <213> Homo sapiens <220> <221> modified_base <222> (1871)..(1873) <223> Wherein N is A, C, G or T <2205 <223> N-Terminal Truncated Telomerase (ver. 2); with Intron Y <400> 51 atgccgcgcg ctccccgctg ccgagccgtg cgctccctgc tgcgcagcca ctaccgcgag 60 gtgctgccgc tggccacgtt cgtgcggcgc ctggggcccc agggctggcg gctggtgcag 120 cgcggggacc cggcggcttt ccgcgcgctg gtggcccagt gcctggtgtg cgtgccctgg 180 gacgcacggc cgcccccccc cgccccctcc ttccgccagg tgggcctccc cggggtcggc 240 gtccggctgg ggttgagggc ggccgggggg aaccagcgac atgcggagag cagcgcaggc 300 gactcagggc gcttcccccg caggtgtcct gcctgaagga gctggtggcc cgagtgctgc 360 agaggetgtg cgagegege gegaagaacg tgetggeett eggettegeg etgetggaeg 420 gggcccgcgg gggccccccc gaggccttca ccaccagcgt gcgcagctac ctgcccaaca 480 cggtgaccga cgcactgcgg gggagcgggg cgtgggggct gctgctgcgc cgcgtgggcg 540 acgacgtgct ggttcacctg ctggcacgct gcgcgctctt tgtgctggtg gctcccagct 600 gcgcctacca ggtgtgcggg ccgccgctgt accagctcgg cgctgccact caggcccggc 660 ccccgccaca cgctagtgga ccccgaaggc gtctgggatg cgaacgggcc tggaaccata 720 gcgtcaggga ggccggggtc cccctgggcc tgccagcccc gggtgcgagg aggcgcgggg 780 gcagtgccag ccgaagtctg ccgttgccca agaggcccag gcgtggcgct gcccctgagc 840 cggagcggac gcccgttggg caggggtcct gggcccaccc gggcaggacg cgtggaccga 900 gtgaccgtgg tttctgtgtg gtgtcacctg ccagacccgc cgaagaagcc acctctttgg 960 agggtgcgct ctctggcacg cgccactccc acccatccgt gggccgccag caccacgcgg 1020 geoceccate cacategegg ceaceaegte cetgggacae geettgteec ceggtgtacg 1080 ccgagaccaa gcacttcctc tactcctcag gcgacaagga gcagctgcgg ccctccttcc 1140 tactcagete tetgaggeee ageetgactg gegeteggag getegtggag accatettte 1200 tgggttccag gccctggatg ccagggactc cccgcaggtt gccccgcctg ccccagcgct 1260 actggcaaat gcggcccctg tttctggagc tgcttgggaa ccacgcgcag tgcccctacg 1320 gggtgctcct caagacgcac tgcccgctgc gagctgcggt caccccagca gccggtgtct 1380 gtgcccggga gaagccccag ggctctgtgg cggcccccga ggaggaggac acagaccccc 1440 gtcgcctggt gcagctgctc cgccagcaca gcagcccctg gcaggtgtac ggcttcgtgc 1500 gggcctgcct gcgccggctg gtgcccccag gcctctgggg ctccaggcac aacgaacgcc 1560 gcttcctcag gaacaccaag aagttcatct ccctggggaa gcatgccaag ctctcgctgc 1620 aggagetgae gtggaagatg agegtgeggg aetgegettg getgegeagg ageceagggg 1680 ttggctgtgt tccggccgca gagcaccgtc tgcgtgagga gatcctggcc aagttcctgc 1740 actggctgat gagtgtgtac gtcgtcgagc tgctcaggtc tttcttttat gtcacggaga 1800

ccacgtttca aaagaacagg ctctttttct accggaagag tgtctggagc aagttgcaaa 1860 gcattggaat nnngacagtc accaggggg ttgaccgccg gactgggcgt ccccagggtt 1920

gactatagga ccaggtgtcc aggtgccctg caagtagagg ggctctcaga ggcgtctggc 1980 tggcatggt ggacgtggcc ccgggcatgg ccttctgcgt gtgctgccgt gggtgccctg 2040 agccctcact gagtcggtgg gggcttgtgg cttcccgtga gcttccccct agtctgttgt 2100 ctggctgagc aagcctcctg aggggctctc tattg <210> 52 <211> 622 <212> PRT <213> Homo sapiens <220> <223> N-Terminal Truncated Telomerase (ver.2); encoded by SEQ ID NO:51 and ORF1 of Intron Y <400> 52 Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Gly Leu Pro Gly Val Gly Val Arg Leu Gly Leu Arg Ala Ala Gly Gly Asn Gln Arg His Ala Glu Ser Ser Ala Gly Asp Ser Gly Arg Phe Pro Arg Arg Ser Cys Leu Lys Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys 120 Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr 155 Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg 165 170 Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu 185 Phe Val Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro 195 200 Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala

100

2135

Ser Gly Pro Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser

Val Arg Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg 245 250 255

Arg Arg Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro 260 265 270

Arg Arg Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly
275 280 285

Ser Trp Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe 290 295 300

Cys Val Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu 305 310 315 320

Gly Ala Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln 325 330 335

His His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp 340 345 350

Thr Pro Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser 355 360 365

Ser Gly Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu 370 375 380

Arg Pro Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu 385 390 395 400

Gly Ser Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu 405 410 415

Pro Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly 420 425 430

Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro 435 440 445

Leu Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys
450 455

Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg 465 470 475 480

Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr 485 490 495

Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp 500 505 510

Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe 515 520 525

Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp 530 540

DIO

Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val 545

Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala 575

Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg 580 585 590

Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe 595 600 605

Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly 610 620

<210> 53 <211> 84 <212> PRT

<213> Homo sapiens

<220>

<223> Splicing Variant of Human Telomerase encoded by
 Intron Y, ORF2, berfore the termination codon.
 SEQ ID NOs: 51,55,59,63,67,71,75,79,83 encode this
 fragment

<400> 53

Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser 1 5 10 15

His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
20 25 30

Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg 35 40 45

Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro 50 60

Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ala Ser Pro Gly Ser Ala 65 70 75 80

Ser Gly Trp Gly

<210> 54

<211> 537

<212> PRT

<213> Homo sapiens

<220>

<223> N-Terminal Truncated Telomerase (ver. 2); encoded by SEQ ID NO:51, with Y intron, ORF2, after the termination codon

	0> 5 Arg		Gly	Gly 5	Thr	Ser	Asp	Met	Arg 10	Arg	Ala	Ala	Gln	Ala 15	Thr
Gln	Gly	Ala	Ser 20	Pro	Ala	Gly	Ser	Cys 25	Leu	Lys	Glu	Leu	Val 30	Ala	Arg
Val	Leu	Gln 35	Arg	Leu	Cys	Glu	Arg 40	Gly	Ala	Lys	Asn	Val 45	Leu	Ala	Phe
Gly	Phe 50	Ala	Leu	Leu	Asp	Gly 55	Ala	Arg	Gly	Gly	Pro 60	Pro	Glu	Ala	Phe
Thr 65	Thr	Ser	Val	Arg	Ser 70	Tyr	Leu	Pro	Asn	Thr 75	Val	Thr	Asp	Ala	Leu 80
Arg	Gly	Ser	Gly	Ala 85	Trp	Gly	Leu	Leu	Leu 90	Arg	Arg	Val	Gly	Asp 95	Asp
Val	Leu	Val	His 100	Leu	Leu	Ala	Arg	Cys 105	Ala	Leu	Phe	Val	Leu 110	Val	Ala
Pro	Ser	Cys 115	Ala	Tyr	Gln	Val	Cys 120	Gly	Pro	Pro	Leu	Tyr 125	Gln	Leu	Gly
Ala	Ala 130	Thr	Gln	Ala	Arg	Pro 135	Pro	Pro	His	Ala	Ser 140	Gly	Pro	Arg	Arg
Arg 145	Leu	Gly	Cys	Glu	Arg 150	Ala	Trp	Asn	His	Ser 155	Val	Arg	Glu	Ala	Gly 160
Val	Pro	Leu	Gly	Leu 165	Pro	Ala	Pro	Gly	Ala 170	Arg	Arg	Arg	Gly	Gly 175	Ser
Ala	Ser	Arg	Ser 180	Leu	Pro	Leu	Pro	Lys 185	Arg	Pro	Arg	Arg	Gly 190	Ala	Ala
Pro	Glu	Pro 195	Glu	Arg	Thr	Pro	Val 200	Gly	Gln	Gly	Ser	Trp 205	Ala	His	Pro
Gly	Arg 210	Thr	Arg	Gly	Pro	Ser 215	Asp	Arg	Gly	Phe	Cys 220	Val	Val	Ser	Pro
225					230		Thr			235					240
				245			Val		250					255	
			260				Arg	265					270		
		275					Phe 280					285			
Gln	Leu 290	Arg	Pro	Ser	Phe	Leu 295	Leu	Ser	Ser	Leu	Arg 300	Pro	Ser	Leu	Thr

Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser Arg Pro Trp 310 Met Pro Gly Thr Pro Arg Leu Pro Arg Leu Pro Gln Arg Tyr Trp 330 Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His Ala Gln Cys 345 Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg Ala Ala Val 355 360 Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln Gly Ser Val 370 Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu Val Gln Leu 390 395 Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser Leu Gly Lys 440 His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met Ser Val Arg 455 Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys Val Pro Ala 465 470 475 Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe Leu His Trp 490 Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe Phe Tyr Val 505 Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr Arg Lys Ser 515 Val Trp Ser Lys Leu Gln Ser Ile Gly 530 <210> 55 <211> 2145 <212> DNA <213> Homo sapiens <220>

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<223> Truncated Protein 1 (ver.2); with Introns Y and 1

<400> 55

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gactcagggc gcttcccccg caggtgtcct gcctgaagga gctggtggcc cgagtgctgc 360
agaggetgtg cgagegegge gegaagaaeg tgetggeett eggettegeg etgetggaeg 420
gggcccgcgg gggccccccc gaggccttca ccaccagcgt gcgcagctac ctgcccaaca 480
cggtgaccga cgcactgcgg gggagcgggg cgtgggggct gctgctgcgc cgcgtgggcq 540
acgacgtgct ggttcacctg ctggcacgct gcgcgctctt tgtgctggtg gctcccagct 600
gcgcctacca ggtgtgcggg ccgccgctgt accagctcgg cgctgccact caggcccggc 660
ccccgccaca cgctagtgga ccccgaaggc gtctgggatg cgaacgggcc tggaaccata 720
gcgtcaggga ggccggggtc cccctgggcc tgccagcccc gggtgcgagg aggcgcgggg 780
gcagtgccag ccgaagtctg ccgttgccca agaggcccag gcgtggcgct gcccctgagc 840
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gtgaccgtgg tttctgtgtg gtgtcacctg ccagacccgc cgaagaagcc acctctttqq 960
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tgggttccag gccctggatg ccagggactc cccgcaggtt gccccgcctg ccccagcgct 1260
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getteeteag gaacaccaag aagtteatet eeetggggaa geatgeeaag etetegetge 1620
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ccacgtttca aaagaacagg ctcttttct accggaagag tgtctggagc aagttgcaaa 1860
gcattggaat cagacagcac ttgaagaggg tgcagctgcg ggagctgtcg gaagcagagg 1920
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gcagagaaaa gagggtggct gtgctttggt ttaacttcct ttttaaccag aagccgagcg 2100
tctcacctcg agggtgaagg cactgttcag cgtgctcaac tacga
                                                                  2145
<210> 56
<211> 704
<212> PRT
<213> Homo sapiens
<220>
<223> Truncated Protein 1 (ver.2); encoded by SEQ ID
     NO:55, with Y Intron ORF1
<400> 56
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Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser

His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly 20 25 30

Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg

Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro

Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Gly Leu Pro Gly Val Gly 65 70

Val Arg Leu Gly Leu Arg Ala Ala Gly Gly Asn Gln Arg His Ala Glu Ser Ser Ala Gly Asp Ser Gly Arg Phe Pro Arg Arg Ser Cys Leu Lys 105 Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys 120 Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly 130 135 Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr 150 155 Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu 185 Phe Val Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro 200 Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala 215 Ser Gly Pro Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser 230 Val Arg Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg 250 Arg Arg Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro 265 Arg Arg Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe 295 Cys Val Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu 305 Gly Ala Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln 330 His His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp 340 345 350 Thr Pro Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser

380

Ser Gly Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu

Arg Pro Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu 405 410 Pro Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly 425 Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro 440 Leu Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys 450 Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr 490 Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe 520 Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val 550 555 Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala 565 570 Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg 585 Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe

DIO

Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg

Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val 625 630 635 640

Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg 645 650 655

Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr 660 665 670

Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Val Ala Val Leu 675 680 685

Trp Phe Thr Phe Leu Phe Asn Gln Lys Pro Ser Val Ser Phe Arg Gly

<210> 57

<211> 619

<212> PRT

<213> Homo sapiens

<220>

<223> Truncated Protein 1 (ver.2): encoded by SEQ ID
 NO:55, with Intron Y ORF2 after the termination
 codon

<400> 57

Gly Arg Pro Gly Gly Thr Ser Asp Met Arg Arg Ala Ala Gln Ala Thr
1 5 10 15

Gln Gly Ala Ser Pro Ala Gly Ser Cys Leu Lys Glu Leu Val Ala Arg 20 25 30

DIS

Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val Leu Ala Phe
35 40

Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro Glu Ala Phe 50 55 60

Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr Asp Ala Leu 65 70 75 80

Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val Gly Asp Asp 85 90 95

Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val Leu Val Ala 100 105 110

Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr Gln Leu Gly
115 120 125

Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly Pro Arg Arg 130 135 140

Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg Glu Ala Gly
145 150 155 160

Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Gly Gly Ser 165 170 175

Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg Gly Ala Ala 180 185 190

Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp Ala His Pro 195 200 205

Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val Val Ser Pro 210 215 220

Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala Leu Ser Gly 225 Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His Ala Gly Pro 250 Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro Cys Pro Pro 265 Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro Ser Leu Thr 295 300 Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser Arg Pro Trp 310 320 Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln Arg Tyr Trp 330 Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg Ala Ala Val 360 Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln Gly Ser Val 370 375 Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe Val Arg Ala 410 Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser Leu Gly Lys 440 His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met Ser Val Arg 455 Asp Cys Ala Trp Leu Arg Ser Pro Gly Val Gly Cys Val Pro Ala 470 Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe Leu His Trp 485 Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe Phe Tyr Val 505

Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr Arg Lys Ser 515 520 525

Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His Leu Lys Arg 535 Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln His Arg Glu 550 555 Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile Pro Lys Pro 570 Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val Gly Ala Arg 585 Thr Phe Arg Arg Glu Lys Arg Val Ala Val Leu Trp Phe Thr Phe Leu 600 605 Phe Asn Gln Lys Pro Ser Val Ser Phe Arg Gly 615 <210> 58 <211> 704 <212> PRT <213> Homo sapiens <220> <223> Truncated Protein 1 (ver.2); encoded by SEQ ID NO:55, with Intron Y ORF3 <400> 58 Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly 20 Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg

Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
50 55 60

Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Pro Pro Arg Cly Arg Arg

Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Pro Pro Arg Gly Arg Arg 65 70 75 80

Pro Ala Gly Val Glu Gly Gly Arg Gly Glu Pro Ala Thr Cys Gly Glu 85 90 95

Gln Arg Arg Leu Arg Ala Leu Pro Pro Gln Val Ser Cys Leu Lys 100 105 110

Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys 115 120 125

Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly 130 135 140

Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr 145 150 155 160 Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Arg
165 170 175

Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu 180 185 190

Phe Val Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro 195 200 205

Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala 210 215 220

Ser Gly Pro Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser 225 230 235 240

Val Arg Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg 245 250 255

Arg Arg Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro 260 265 270

Arg Arg Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly 275 280 285

Ser Trp Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe 290 295 300

Cys Val Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu 305 310 315 320

Gly Ala Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln 325 330 335

His His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp 340 345 350

Thr Pro Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser 355 360 365

Ser Gly Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu 370 375 380

Arg Pro Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu 385 390 395 400

Gly Ser Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu 405 410 415

Pro Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly
420 425 430

Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro 435 440 445

Leu Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys 450 455 460 Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gly Leu Trp 510

Gly Phe Val Arg Ala Cys Leu Arg Arg Phe Leu Arg Arg Leu Arg Slo Thr Ser Pro Trp Gly Leu Trp 510

Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Arg Leu Gln Glu Leu Thr Trp 530

Lys Met Ser Val Arg Arg Ala Glu His Arg Leu Arg Arg Leu Arg Arg Ser Pro Gly Val 560

Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Arg Leu Arg Arg Arg Ser Pro Gly Val 575

Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Arg Arg Leu Phe Ser Pro Pro Pro Ser Pro Pro Ser P

DID

Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe 595 600 605

Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg 610 620

Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val 625 630 635 640

Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg 645 650 655

Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr 660 665 670

Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Val Ala Val Leu 675 680 685

Trp Phe Thr Phe Leu Phe Asn Gln Lys Pro Ser Val Ser Phe Arg Gly 690 695 700

<210> 59

<211> 2645

<212> DNA

<213> Homo sapiens

<220>

<223> Truncated Protein 2 (ver.2); with Intron Y and Alpha

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Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Gly Leu Pro Gly Val Gly 65 70 75 80

Val Arg Leu Gly Leu Arg Ala Ala Gly Gly Asn Gln Arg His Ala Glu 85 90 95

Ser Ser Ala Gly Asp Ser Gly Arg Phe Pro Arg Arg Ser Cys Leu Lys 100 105 110

Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys 115 120 125

Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly 130 135 140

Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr 145 150 155 160

Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Arg 165 170 175

Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu 180 185 190

Phe Val Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro 195 200 205

Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala 210 215 220

Ser Gly Pro Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser 225 230 235 240

Val Arg Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg 245 250 255

Arg Arg Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro 260 265 270

Arg Arg Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly 275 280 285

Ser Trp Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe 290 295 300

Cys Val Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu 305 310 315 320

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D10

610

Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg

Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val 630 635 Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr 665 Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu 680 Thr Ser Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala 695 Arg Arg Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile 715 His Arg Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro 730 Pro Pro Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His Gly His Val Arg Lys Ala Phe Lys Ser His Val Leu Arg Pro 790 795

Val Pro Gly Asp Pro Ala Gly Leu His Pro Leu His Ala Ala Leu Gln 805

Pro Val Leu Arg Arg His Gly Glu Gln Ala Val Cys Gly Asp Ser Ala

Gly Arg Ala Ala Pro Ala Phe Val Gly 835

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<212> PRT

<213> Homo sapiens

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Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro Glu Ala Phe 50 55 60

Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr Asp Ala Leu 65 70 75 80

Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val Gly Asp Asp 85 90 95

Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val Leu Val Ala 100 105 110

Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr Gln Leu Gly
115 120 125

Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly Pro Arg Arg 130 135 140

Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg Glu Ala Gly 145 150 155 160

Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Gly Gly Ser 165 170 175

Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg Gly Ala Ala 180 185 190

Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp Ala His Pro 195 200 205

Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val Val Ser Pro 210 215 220

Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala Leu Ser Gly 225 230 235 240

Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His Ala Gly Pro 245 250 255

Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro Cys Pro Pro 260 265 270

Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly Asp Lys Glu 275 280 285

Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro Ser Leu Thr 290 295 300

Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser Arg Pro Trp 305 310 315 320

Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln Arg Tyr Trp 325 330 335

Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg Ala Ala Val 360 Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu Val Gln Leu 390 Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe Val Arg Ala 405 410 Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser Arg His Asn 420 Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser Leu Gly Lys 440 His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met Ser Val Arg 450 455 Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe Leu His Trp 490 Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe Phe Tyr Val 505 Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr Arg Lys Ser 515 520 Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln His Arg Glu 545 Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile Pro Lys Pro 570 Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val Gly Ala Arg 585 Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser Arg Val Lys 600 Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Pro Gly Leu 615 Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg Ala Trp Arg 625 630

Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro Glu Leu Tyr 650 Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln Asn Thr Tyr 680 Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His Gly His Val 695 Arg Lys Ala Phe Lys Ser His Val Leu Arg Pro Val Pro Gly Asp Pro 710 Ala Gly Leu His Pro Leu His Ala Ala Leu Gln Pro Val Leu Arg Arg 730 His Gly Glu Gln Ala Val Cys Gly Asp Ser Ala Gly Arg Ala Ala Pro 745 Ala Phe Val Gly 755 <210> 62 <211> 841 <212> PRT <213> Homo sapiens <223> Truncated Protein 2 (ver.2); encoded by SEQ ID NO: 59 with Intron Y ORF3 Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly 25

Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg 35 40 45

Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro 50 55 60

Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Pro Pro Arg Gly Arg Arg 65 70 75 80

Pro Ala Gly Val Glu Gly Gly Arg Gly Glu Pro Ala Thr Cys Gly Glu 85 90 95

Gln Arg Arg Leu Arg Ala Leu Pro Pro Gln Val Ser Cys Leu Lys 100 105 110

Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys 115 120 125 Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly 130 135 Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr 150 Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Arg 170 Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu 180 Phe Val Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala 210 220 Ser Gly Pro Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser 230 Val Arg Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro 265 Arg Arg Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly 280 Ser Trp Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu 310 315 Gly Ala Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln 325 330 His His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp 345 Thr Pro Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu 375 380 Arg Pro Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu 385 390 395 Gly Ser Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu 410 Pro Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly 420 425 430

D10

Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro 440 Leu Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg 470 475 Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr 490 Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe 520 Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg 585 Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe 595 Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg 650 Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr 665 Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu 675 680 Thr Ser Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala 695 Arg Arg Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile 705 His Arg Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro 730

Pro Pro Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp

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740 745 750
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Thr Ile Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys
755 760 765

Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala 770 780

Ala His Gly His Val Arg Lys Ala Phe Lys Ser His Val Leu Arg Pro 785 790 795 800

Val Pro Gly Asp Pro Ala Gly Leu His Pro Leu His Ala Ala Leu Gln 805 810 815

Pro Val Leu Arg Arg His Gly Glu Gln Ala Val Cys Gly Asp Ser Ala 820 825 830

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                                                                   3500
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<212> PRT
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<220>
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His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
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Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
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DID

65

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Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Gly Leu Pro Gly Val Gly

Val Arg Leu Gly Leu Arg Ala Ala Gly Gly Asn Gln Arg His Ala Glu Ser Ser Ala Gly Asp Ser Gly Arg Phe Pro Arg Arg Ser Cys Leu Lys 105 Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys 120 Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly 135 Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr 150 Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Arg 170 Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu 180 185 Phe Val Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala 210 Ser Gly Pro Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg 250 Arg Arg Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro 260 265 Arg Arg Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly 280 Ser Trp Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe 290 Cys Val Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln 325 330 His His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp 345 Thr Pro Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu

Arg Pro Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu

Gly Ser Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu 405 410 415

390

Pro Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly 420 425 430

Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro
435 440 445

Leu Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys 450 455 460

Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg 465 470 475 480

Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr 485 490 495

Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp 500 505 510

Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe 515 520 525

Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp 530 540

Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val 545 550 555 560

Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala 565 570 575

Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg 580 585 590

Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe 595 600 605

Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg 610 615 620

Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val 625 630 635 640

Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg 645 650 655

Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr 660 665 670

Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu 675 680 685

Thr Ser Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala 690 695 700

Arg Arg Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile 705 His Arg Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro 730 Pro Pro Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp 745 Thr Ile Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys 760 Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala 775 Ala His Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu Thr Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu Thr Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Leu Asn Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys 840 His His Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly 850 855 Ile Pro Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu 890 Leu Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr 905 His Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr 915 920 Gly Cys Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly 950 955 Leu Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val 965 970 Gln Ser Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu 985 Thr Phe Asn Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu 1000 1005

Phe Gly Val Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln 1010 1015 1020

Val Asn Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu 1025 1030 1035 1040

Leu Gln Ala Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe His 1045 1050 1055

Gln Gln Val Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp 1060 1065 1070

Thr Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala Gly Met Ser 1075 1080 1085

Leu Gly Ala Lys Gly Ala Ala Gly Pro Leu Pro Ser Glu Ala Val Gln 1090 1095 1100

Trp Leu Cys His Gln Ala Phe Leu Leu Lys Leu Thr Arg His Arg Val 1105 1110 1115 1120

Thr Tyr Val Pro Leu Leu Gly Ser Leu Arg Thr Ala Gln Thr Gln Leu 1125 1130 1135

Ser Arg Lys Leu Pro Gly Thr Thr Leu Thr Ala Leu Glu Ala Ala 1140 1145 1150

Asn Pro Ala Leu Pro Ser Asp Phe Lys Thr Ile Leu Asp 1155 1160 1165

<210> 65

<211> 1081

<212> PRT

<213> Homo sapiens

<220>

<223> Reference Protein (ver.2); encoded by SEQ ID NO:63
 with Intron Y ORF2 after the termination codon

<400> 65

Gly Arg Pro Gly Gly Thr Ser Asp Met Arg Arg Ala Ala Gln Ala Thr
1 5 10 15

Gln Gly Ala Ser Pro Ala Gly Ser Cys Leu Lys Glu Leu Val Ala Arg 20 25 30

Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val Leu Ala Phe 35 40 45

Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro Glu Ala Phe 50 55 60

Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr Asp Ala Leu 65 70 75 80

Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val Gly Asp Asp 85 90 95

Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly Pro Arg Arg 135 Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg Glu Ala Gly 150 Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg Gly Gly Ser 170 Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp Ala His Pro 200 Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val Val Ser Pro 210 220 Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala Leu Ser Gly 230 235 Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His Ala Gly Pro 245 250 Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly Asp Lys Glu 280 Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro Ser Leu Thr 295 Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser Arg Pro Trp 310 315 Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His Ala Gln Cys 345 Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg Ala Ala Val 355 Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln Gly Ser Val

D10

385

395

Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu Val Gln Leu

Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe Val Arg Ala 410 Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser Leu Gly Lys 440 His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met Ser Val Arg 455 Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe Leu His Trp 490 Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe Phe Tyr Val 500 Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln His Arg Glu 550 Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile Pro Lys Pro 570 Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile Pro Gln Asp 665 Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln Asn Thr Tyr 675 680 Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His Gly His Val

Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu Thr Asp Leu Gln Pro

D10

1020

Gly Ala Ala Gly Pro Leu Pro Ser Glu Ala Val Gln Trp Leu Cys His

Gln Ala Phe Leu Leu Lys Leu Thr Arg His Arg Val Thr Tyr Val Pro 1025 1030 Leu Leu Gly Ser Leu Arg Thr Ala Gln Thr Gln Leu Ser Arg Lys Leu 1050 Pro Gly Thr Thr Leu Thr Ala Leu Glu Ala Ala Ala Asn Pro Ala Leu 1065 Pro Ser Asp Phe Lys Thr Ile Leu Asp 1075 1080 <210> 66 <211> 1165 <212> PRT <213> Homo sapiens <220> <223> Reference Protein (ver.2); encoded by SEQ ID NO:63 with Intron Y ORF3 <400> 66 Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser 10 15 His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Pro Pro Arg Gly Arg Arg Pro Ala Gly Val Glu Gly Gly Arg Gly Glu Pro Ala Thr Cys Gly Glu Gln Arg Arg Leu Arg Ala Leu Pro Pro Gln Val Ser Cys Leu Lys 105 Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys 120 Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly 135 Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr 145 150 Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg 170

Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu

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Leu	Tyr 210		Leu	Gly	Ala	Ala 215	Thr	Gln	Ala	Arg	Pro 220	Pro	Pro	His	Ala
Ser 225	Gly	Pro	Arg	Arg	Arg 230	Leu	Gly	Cys	Glu	Arg 235	Ala	Trp	Asn	His	Ser 240
Val	Arg	Glu	Ala	Gly 245	Val	Pro	Leu	Gly	Leu 250	Pro	Ala	Pro	Gly	Ala 255	Arg
Arg	Arg	Gly	Gly 260	Ser	Ala	Ser	Arg	Ser 265	Leu	Pro	Leu	Pro	Lys 270	Arg	Pro
Arg	Arg	Gly 275	Ala	Ala	Pro	Glu	Pro 280	Glu	Arg	Thr	Pro	Val 285	Gly	Gln	Gly
Ser	Trp 290	Ala	His	Pro	Gly	Arg 295	Thr	Arg	Gly	Pro	Ser 300	Asp	Arg	Gly	Phe
Cys 305	Val	Val	Ser	Pro	Ala 310	Arg	Pro	Ala	Glu	Glu 315	Ala	Thr	Ser	Leu	Glu 320
Gly	Ala	Leu	Ser	Gly 325	Thr	Arg	His	Ser	His 330	Pro	Ser	Val	Gly	Arg 335	Gln
His	His	Ala	Gly 340	Pro	Pro	Ser	Thr	Ser 345	Arg	Pro	Pro	Arg	Pro 350	Trp	Asp
Thr	Pro	Cys 355	Pro	Pro	Val	Tyr	Ala 360	Glu	Thr	Lys	His	Phe 365	Leu	Tyr	Ser
Ser	Gly 370	Asp	Lys	Glu	Gln	Leu 375	Arg	Pro	Ser	Phe	Leu 380	Leu	Ser	Ser	Leu
Arg 385	Pro	Ser	Leu	Thr	Gly 390	Ala	Arg	Arg	Leu	Val 395	Glu	Thr	Ile	Phe	Leu 400
Gly	Ser	Arg	Pro	Trp 405	Met	Pro	Gly	Thr	Pro 410	Arg	Arg	Leu	Pro	Arg 415	Leu
Pro	Gln	Arg	Tyr 420	Trp	Gln	Met	Arg	Pro 425	Leu	Phe	Leu	Glu	Leu 430	Leu	Gly
Asn	His	Ala 435	Gln	Cys	Pro	Tyr	Gly 440	Val	Leu	Leu	Lys	Thr 445	His	Cys	Pro
Leu	Arg 450	Ala	Ala	Val	Thr	Pro 455	Ala	Ala	Gly	Val	Cys 460	Ala	Arg	Glu	Lys
Pro 465	Gln	Gly	Ser	Val	Ala 470	Ala	Pro	Glu	Glu	Glu 475	Asp	Thr	Asp	Pro	Arg 480
Arg	Leu	Val	Gln	Leu 485	Leu	Arg	Gln	His	Ser 490	Ser	Pro	Trp	Gln	Val 495	Tyr

Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe 520 Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp 535 Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala 570 Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val 630 Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg 645 650 Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu 680 Thr Ser Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile 715 His Arg Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro 730 Pro Pro Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp 745 Thr Ile Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys 755 Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala 775 Ala His Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu

795

Thr Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu 810 Thr Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Leu 825 Asn Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys 840 His His Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly 855 Ile Pro Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr 870 Gly Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu 890 Leu Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly Cys Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu 935 Asp Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly 950 Leu Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val 965 Gln Ser Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu Thr Phe Asn Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu 1000 Phe Gly Val Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln 1015 Val Asn Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu 1035 Leu Gln Ala Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe His 1045 1050 Gln Gln Val Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp 1065 Thr Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala Gly Met Ser 1075 Leu Gly Ala Lys Gly Ala Ala Gly Pro Leu Pro Ser Glu Ala Val Gln 1095

>10

Trp Leu Cys His Gln Ala Phe Leu Leu Lys Leu Thr Arg His Arg Val

Thr Tyr Val Pro Leu Leu Gly Ser Leu Arg Thr Ala Gln Thr Gln Leu 1125 1130 1135

Ser Arg Lys Leu Pro Gly Thr Thr Leu Thr Ala Leu Glu Ala Ala Ala 1140 1145 1150

Asn Pro Ala Leu Pro Ser Asp Phe Lys Thr Ile Leu Asp 1155 1160 1165

<210> 67 <211> 3173

<212> DNA

<213> Homo sapiens

<220>

<400> 67

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tecacaggge etggegeace ttegtgetge gtgtgeggge ecaggaeeeg eegeetgage 2220
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ggtcagatgc cacagggtgc ccctcgtccc atctggggct gagcacaaat gcatctttct 3120
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<210> 68
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<212> PRT
<213> Homo sapiens
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<223> Truncated Protein 3 (ver.2); encoded by SEQ ID
      NO:67 with Intron Y ORF1
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His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
                             40
Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Gly Leu Pro Gly Val Gly
                                         75
Val Arg Leu Gly Leu Arg Ala Ala Gly Gly Asn Gln Arg His Ala Glu
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155

160

Ser Ser Ala Gly Asp Ser Gly Arg Phe Pro Arg Arg Ser Cys Leu Lys

Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys

Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly

Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr

135

150

105

100

115

Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu 185 Phe Val Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro 200 Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg 250 Arg Arg Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly 280 Ser Trp Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe 290 295 Cys Val Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln 330 His His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser 360 Ser Gly Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu 390 395 Gly Ser Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu 405 410 Pro Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly 420 425 Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro 435 Leu Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys 455

Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg

D10

Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe

Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg 610 620

Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val 625 630 635 640

Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg 645 650 655

Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr 660 665 670

Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu 675 680 685

Thr Ser Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala 690 695 700

Arg Arg Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile 705 710 715 720

His Arg Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro 725 730 735

Pro Pro Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp 740 745 750

Thr Ile Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys 755 760 765

Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala 770 780

Ala His Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu Thr Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu 810 Thr Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Leu 825 Asn Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys 835 His His Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly 855 Ile Pro Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr 870 Gly Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr 910 His Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr 920 Gly Cys Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu 930 935 Asp Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly 945 Leu Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val 970 Gln Ser Asp Tyr Ser Arg 980

<210> 69

<211> 897

<212> PRT

<213> Homo sapiens

<220>

<223> Truncated Protein 3 (ver.2); encoded by SEQ ID NO:67 with Intron Y ORF2 after the termination codon

<400> 69

Gly Arg Pro Gly Gly Thr Ser Asp Met Arg Arg Ala Ala Gln Ala Thr
1 5 10 15

Gln Gly Ala Ser Pro Ala Gly Ser Cys Leu Lys Glu Leu Val Ala Arg 20 25 30

Val	Leu	Gln 35	Arg	Leu	. Cys	Glu	ı Arg 40		Ala	. Lys	Asn	Val 45		Ala	Phe
Gly	Phe 50	Ala	Leu	Leu	Asp	Gly 55		. Arg	Gly	Gly	Pro 60		Glu	Ala	Phe
Thr 65	Thr	Ser	Val	Arg	Ser 70		Leu	Pro	Asn	Thr 75		Thr	Asp	Ala	Leu 80
Arg	Gly	Ser	Gly	Ala 85		Gly	Leu	Leu	Leu 90		Arg	Val	Gly	Asp 95	Asp
Val	Leu	Val	His 100		Leu	Ala	Arg	Cys 105		Leu	Phe	Val	Leu 110	Val	Ala
Pro	Ser	Cys 115		Tyr	Gln	Val	Cys 120	Gly	Pro	Pro	Leu	Tyr 125		Leu	Gly
Ala	Ala 130	Thr	Gln	Ala	Arg	Pro 135	Pro	Pro	His	Ala	Ser 140	Gly	Pro	Arg	Arg
Arg 145	Leu	Gly	Cys	Glu	Arg 150	Ala	Trp	Asn	His	Ser 155	Val	Arg	Glu	Ala	Gly 160
Val	Pro	Leu	Gly	Leu 165	Pro	Ala	Pro	Gly	Ala 170	Arg	Arg	Arg	Gly	Gly 175	Ser
Ala	Ser	Arg	Ser 180	Leu	Pro	Leu	Pro	Lys 185	Arg	Pro	Arg	Arg	Gly 190	Ala	Ala
Pro	Glu	Pro 195	Glu	Arg	Thr	Pro	Val 200	Gly	Gln	Gly	Ser	Trp 205	Ala	His	Pro
Gly	Arg 210	Thr	Arg	Gly	Pro	Ser 215	Asp	Arg	Gly	Phe	Cys 220	Val	Val	Ser	Pro
Ala 225	Arg	Pro	Ala	Glu	Glu 230	Ala	Thr	Ser	Leu	Glu 235	Gly	Ala	Leu	Ser	Gly 240
Thr	Arg	His	Ser	His 245	Pro	Ser	Val	Gly	Arg 250	Gln	His	His	Ala	Gly 255	Pro
Pro	Ser	Thr	Ser 260	Arg	Pro	Pro	Arg	Pro 265	Trp	Asp	Thr	Pro	Cys 270	Pro	Pro
Val	Tyr	Ala 275	Glu	Thr	Lys	His	Phe 280	Leu	Tyr	Ser	Ser	Gly 285	Asp	Lys	Glu
Gln	Leu 290	Arg	Pro	Ser	Phe	Leu 295	Leu	Ser	Ser	Leu	Arg 300	Pro	Ser	Leu	Thr
Gly 305	Ala	Arg	Arg	Leu	Val 310	Glu	Thr	Ile	Phe	Leu 315	Gly	Ser	Arg	Pro	Trp 320
Met	Pro	Gly	Thr	Pro 325	Arg	Arg	Leu	Pro	Arg 330	Leu	Pro	Gln	Arg	Tyr 335	Trp
Gln	Met	Arg	Pro	Leu	Phe	Leu	Glu	Leu	Leu	Gly	Asn	His	Ala	Gln	Cys

DIO

Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg Ala Ala Val 360 Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu Val Gln Leu 390 Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe Val Arg Ala 405 Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser Leu Gly Lys 440 His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met Ser Val Arg 450 Asp Cys Ala Trp Leu Arg Ser Pro Gly Val Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe Leu His Trp 490 Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe Phe Tyr Val 505 Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr Arg Lys Ser 515 Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln His Arg Glu 550 Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile Pro Lys Pro 570 Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val Gly Ala Arg 585 Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser Arg Val Lys 595 600 Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Pro Gly Leu 615 Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg Ala Trp Arg 625 Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro Glu Leu Tyr 645 650

Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln Asn Thr Tyr 680 Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His Gly His Val 695 Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu Thr Asp Leu Gln Pro 710 Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu Thr Ser Pro Leu Arg 730 Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu Asn Glu Ala Ser Ser 740 Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys His His Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly Ile Pro Gln Gly Ser 770 Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly Asp Met Glu Asn 790 Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu Leu Arg Leu Val 805 810 Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly Cys Val Val Asn 840 Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp Glu Ala Leu Gly 855 Gly Thr Ala Phe Val Gln Met Pro Ala His Gly Leu Phe Pro Trp Cys 875 Gly Leu Leu Asp Thr Arg Thr Leu Glu Val Gln Ser Asp Tyr Ser 890

Arg

<210> 70

<211> 982

<212> PRT

<213> Homo sapiens

<220>

<223> Truncated Protein 3 (Ver.2); encoded by SEQ ID NO:67 with Intron Y ORF3

<400> 70 Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser 10 His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly 25 Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Pro Pro Arg Gly Arg Arg Pro Ala Gly Val Glu Gly Gly Arg Gly Glu Pro Ala Thr Cys Gly Glu Gln Arg Arg Leu Arg Ala Leu Pro Pro Gln Val Ser Cys Leu Lys 100 Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys 120 Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly 135 Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr 150 Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg 170 Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu

Phe Val Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro 195 200 205

Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala 210 215 220

Ser Gly Pro Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser 230 235 240

Val Arg Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg 245 250 255

Arg Arg Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro 260 265 270

Arg Arg Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly 275 280 285

Ser Trp Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe 290 295 300

Cys Val Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu 305 Gly Ala Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln 325 330 His His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp 345 Thr Pro Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu 375 Arg Pro Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu 395 Gly Ser Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu 410 Pro Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly 420 425 Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys 450 Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr 490 Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp 505 Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe 520 Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp 530 Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val 550 555 Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg 585 Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe

595

Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val 630 635 Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg 650 Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr 660 Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala 695 Arg Arg Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile 710 His Arg Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala 770 Ala His Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu Thr Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu 810 Thr Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Leu Asn Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys 840 His His Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly Ile Pro Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr 870 875 Gly Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu 885 Leu Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr

905

His Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr

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915 920 925
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Gly Cys Val Val Asn Leu Sarg Lys Thr Val Val Asn Phe Pro Val Glu
Asp Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Gln Met Pro Ala His Gly
945
Leu Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val

970

Gln Ser Asp Tyr Ser Arg

<210> 71
<211> 3466
<212> DNA
<213> Homo sapiens
<220>
<223> Altered C-Terminus Protein (ver.2); with Introns
Y, Alpha, Beta and 3

D/O <400> 71

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<210> 72
<211> 1130
<212> PRT
<213> Homo sapiens
<220>
<223> Altered C-Terminus Protein (ver.2); encoded by SEQ
     ID NO:71 with Intron Y ORF1
<400> 72
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Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser

His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly

Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg 40

Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro

Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Gly Leu Pro Gly Val Gly 70

Val Arg Leu Gly Leu Arg Ala Ala Gly Gly Asn Gln Arg His Ala Glu

Ser Ser Ala Gly Asp Ser Gly Arg Phe Pro Arg Arg Ser Cys Leu Lys

Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys

D10

Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly 135 Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr 150 155 Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu 185 Phe Val Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser 235 Val Arg Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg 250 Arg Arg Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro 260 Arg Arg Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe 290 Cys Val Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu 310 Gly Ala Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln 325 330 His His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser 360 Ser Gly Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu 370 Arg Pro Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu 395 Gly Ser Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu 405 Pro Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly 420 425 430

Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys 455 Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg 470 Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr 490 Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp 505 Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe 520 Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val 550 555 Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala 570 Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg 580 Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe 600 Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg 615 Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val 630 640 Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg 650 Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu 680 Thr Ser Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala 690 695 Arg Arg Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile 715 His Arg Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro 725 730

DIO

Pro Pro Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys 760 Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu 795 Thr Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu Thr Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Leu 825 Asn Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys His His Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly Ile Pro Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr 870 Gly Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr 900 His Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr 920 Gly Cys Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu 935 Asp Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly Leu Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val 970 Gln Ser Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu 980 985 Thr Phe Asn Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu 1000 Phe Gly Val Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln 1010 Val Asn Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu 1030

Leu Gln Ala Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe His

Gln Gln Val Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp 1060 1065 1070

Thr Ala Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala Glu Glu 1075 1080 1085

Glu Asn Ile Leu Val Val Thr Pro Ala Val Leu Gly Ser Gly Gln Pro 1090 1095 1100

Glu Met Glu Pro Pro Arg Arg Pro Ser Gly Val Gly Ser Phe Pro Val 1105 1110 1115 1120

Ser Pro Gly Arg Gly Val Gly Leu Gly Leu 1125 1130

<210> 73

<211> 1045

<212> PRT

<213> Homo sapiens

<220>

<223> Altered C-Terminus Protein (ver.2); encoded by SEQ ID NO:71 with Intron Y ORF2 after the termination codon

<400> 73

Gly Arg Pro Gly Gly Thr Ser Asp Met Arg Arg Ala Ala Gln Ala Thr
1 5 10 15

Gln Gly Ala Ser Pro Ala Gly Ser Cys Leu Lys Glu Leu Val Ala Arg 20 25 30

Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val Leu Ala Phe
35 40 45

Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro Glu Ala Phe 50 55 60

Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr Asp Ala Leu 65 70 75 80

Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val Gly Asp Asp 85 90 95

Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val Leu Val Ala
100 105 110

Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr Gln Leu Gly
115 120 125

Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly Pro Arg Arg 130 135 140

Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg Glu Ala Gly
145 150 155 160

Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Gly Ala Ala 180 Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp Ala His Pro 200 Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His Ala Gly Pro 250 Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro Cys Pro Pro 265 Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly Asp Lys Glu 275 280 Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser Arg Pro Trp 310 315 Met Pro Gly Thr Pro Arg Leu Pro Arg Leu Pro Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His Ala Gln Cys 345 Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg Ala Ala Val 360 Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln Gly Ser Val 375 Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu Val Gln Leu 385 390 Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe Val Arg Ala 410 Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser Arg His Asn 420 Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser Leu Gly Lys

450

460

His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met Ser Val Arg

Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe Leu His Trp 490 Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe Phe Tyr Val 500 505 Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr Arg Lys Ser 520 Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln His Arg Glu 550 Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val Gly Ala Arg 585 Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser Arg Val Lys 600 Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg Ala Trp Arg 625 635 Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His Gly His Val 695 Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu Thr Asp Leu Gln Pro 710 Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu Thr Ser Pro Leu Arg 730 Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu Asn Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys His His Ala Val Arg 760

Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly Ile Pro Gln Gly Ser

770 775 780

Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly Asp Met Glu Asn 785 790 795 800

Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu Leu Arg Leu Val 805 810 815

Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His Ala Lys Thr Phe 820 825 830

Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly Cys Val Val Asn 835 840 845

Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp Glu Ala Leu Gly 850 855 860

Gly Thr Ala Phe Val Gln Met Pro Ala His Gly Leu Phe Pro Trp Cys 865 870 875 880

Gly Leu Leu Asp Thr Arg Thr Leu Glu Val Gln Ser Asp Tyr Ser 885 890 895

Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu Thr Phe Asn Arg Gly
900 905 910

Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu Phe Gly Val Leu Arg 915 920 925

Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln Val Asn Ser Leu Gln 930 935 940

Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu Gln Ala Tyr Arg 945 950 955 960

Phe His Ala Cys Val Leu Gln Leu Pro Phe His Gln Gln Val Trp Lys 965 970 975

Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp Thr Ala Ser Leu Cys 980 985 990

Tyr Ser Ile Leu Lys Ala Lys Asn Ala Glu Glu Glu Asn Ile Leu Val 995 1000 1005

Val Thr Pro Ala Val Leu Gly Ser Gly Gln Pro Glu Met Glu Pro Pro 1010 1015 1020

Arg Arg Pro Ser Gly Val Gly Ser Phe Pro Val Ser Pro Gly Arg Gly 1025 1030 1035 1040

Val Gly Leu Gly Leu 1045

<210> 74

<211> 1130

<212> PRT

<213> Homo sapiens

<220>

<223> Altered C-Terminus Protein (ver.2); encoded by SEQ ID NO:71 with Intron Y ORF3

Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser 1.0

His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly 25

Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg

Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro

Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Pro Pro Arg Gly Arg Arg

Pro Ala Gly Val Glu Gly Gly Arg Gly Glu Pro Ala Thr Cys Gly Glu

Gln Arg Arg Leu Arg Ala Leu Pro Pro Gln Val Ser Cys Leu Lys 100

Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys

Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly 130

Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr 150

Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg 170

Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu

Phe Val Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro 200

Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala 210 215

Ser Gly Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser 235

Val Arg Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg

Arg Arg Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro 265

Arg Arg Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly

Ser Trp Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu 310 315 Gly Ala Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln 325 His His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp 345 Thr Pro Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu 410 Pro Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly 420 Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg 470 Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr 490 Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe 520 Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp 530 Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val 555 Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala 565 Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg 580 585

Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg 615 Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val 630 635 Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr 665 Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile 710 His Arg Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp 740 Thr Ile Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala 775 Ala His Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu Thr Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu 810 Thr Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Leu 820 825 Asn Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys His His Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly 850 Ile Pro Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr 870 875

Gly Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu

Leu Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr 905 His Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr 915 920 Gly Cys Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu 935 Asp Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly 950 Leu Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val Gln Ser Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu 985 Thr Phe Asn Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu Phe Gly Val Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln Val Asn Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu 1025 1035 Leu Gln Ala Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe His 1045 1050 Gln Gln Val Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp 1060 Thr Ala Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala Glu Glu Glu Asn Ile Leu Val Val Thr Pro Ala Val Leu Gly Ser Gly Gln Pro 1095 Glu Met Glu Pro Pro Arg Pro Ser Gly Val Gly Ser Phe Pro Val 1105 1110 Ser Pro Gly Arg Gly Val Gly Leu Gly Leu 1125

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and Beta

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D10

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His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
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Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
     50
Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Gly Leu Pro Gly Val Gly
Val Arg Leu Gly Leu Arg Ala Ala Gly Gly Asn Gln Arg His Ala Glu
Ser Ser Ala Gly Asp Ser Gly Arg Phe Pro Arg Arg Ser Cys Leu Lys
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Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys
                            120
Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly
    130
                        135
Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr
                    150
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Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg
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Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu
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Phe Val Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro
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                            200
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D10

Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly Pro Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro 260 265 Arg Arg Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe 295 Cys Val Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu 315 Gly Ala Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln 330 His His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu 370 Arg Pro Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu 390 Gly Ser Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu 405 410 Pro Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly 425 Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro 440 Leu Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys 455 Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg 475 Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr 495

Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp

Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe

Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp 540 Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val 550 Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala 565 Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg 585 Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe 600 Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg 615 Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val 635 Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg 650 Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr 660 Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala 690 Arg Arg Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro 725 730 Pro Pro Glu Leu Tyr Phe Val Lys Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val 760 Val Gln Lys Ala Ala His Gly His Val Arg Lys Ala Phe Lys Ser His 775 Val Ser Thr Leu Thr Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala 795 His Leu Gln Glu Thr Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln 805 Ser Ser Ser Leu Asn Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu 820 825 830

Arg	Phe	835	Cys	s His	His	s Ala	a Val 840		g Ile	e Arg	g Gly	7 Lys 845		ту1	c Va
Gln	Суs 850	Glr	n Gly	⁄ Il∈	Pro	855		/ Sei	: Ile	e Lei	860		Let	ı Lev	і Су
Ser 865	Leu	Cys	Tyr	Gly	870		Glu	ı Asr	ı Lys	s Leu 875		e Ala	Gly	/ Ile	880
Arg	Asp	Gly	Leu	Leu 885		Arg	, Leu	ı Val	. Asp	p Asp	Phe	e Leu	Leu	Val 895	
Pro	His	Leu	Thr 900		Ala	Lys	Thr	Phe 905		ı Arg	Thr	Leu	Val 910	_	gly
Val	Pro	Glu 915	Tyr	Gly	Cys	Val	Val 920		Let	ı Arg	Lys	Thr 925		Val	Asr
Phe	Pro 930	Val	Glu	Asp	Glu	Ala 935		Gly	Gly	/ Thr	Ala 940		Val	Gln	Met
Pro 945	Ala	His	Gly	Leu	Phe 950	Pro	Trp	Cys	Gly	7 Leu 955	Leu	Leu	Asp	Thr	Arg 960
Thr	Leu	Glu	Val	Gln 965	Ser	Asp	Tyr	Ser	Ser 970	Tyr	Ala	Arg	Thr	Ser 975	
Arg	Ala	Ser	Leu 980	Thr	Phe	Asn	Arg	Gly 985	Phe	. Lys	Ala	Gly	Arg 990	Asn	Met
Arg	Arg	Lys 995	Leu	Phe	Gly		Leu 1000	Arg	Leu	Lys		His 1005	Ser	Leu	Phe
Leu 1	Asp L010	Leu	Gln	Val	Asn	Ser 1015	Leu	Gln	Thr	Val	Cys 1020	Thr	Asn	Ile	Tyr
Lys 1025	Ile	Leu	Leu		Gln 1030	Ala	Tyr	Arg		His 1035	Ala		Val		Gln 1040
Leu	Pro	Phe		Gln 1045	Gln	Val	Trp		Asn 1050	Pro	Thr	Phe		Leu 1055	Arg
Val	Ile	Ser	Asp 1060	Thr	Ala	Ser		Cys 1065	Tyr	Ser	Ile		Lys 1070	Ala	Lys
Asn	Ala 1	Gly .075	Met	Ser	Leu		Ala L080	Lys	Gly	Ala		Gly 1085	Pro	Leu	Pro
Ser 1	Glu 090	Ala	Val	Gln		Leu .095	Cys	His	Gln	Ala	Phe	Leu	Leu	Lys	Leu
Thr 1105	Arg	His	Arg	Val 1	Thr .110	Tyr	Val	Pro		Leu 1115	Gly	Ser	Leu		Thr 120

Ala Gln Thr Gln Leu Ser Arg Lys Leu Pro Gly Thr Thr Leu Thr Ala 1125 1130 1135

Leu Glu Ala Ala Asn Pro Ala Leu Pro Ser Asp Phe Lys Thr Ile 1140 1145 Leu Asp <210> 77 <211> 1069 <212> PRT <213> Homo sapiens <220> <223> Protein Lacking Motif A (ver.2); encoded by SEQ ID NO:75 with Intron Y ORF2 after the termination codon <400> 77 Gly Arg Pro Gly Gly Thr Ser Asp Met Arg Arg Ala Ala Gln Ala Thr 5 10 Gln Gly Ala Ser Pro Ala Gly Ser Cys Leu Lys Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr Asp Ala Leu 70 Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val Leu Val Ala 105 Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr Gln Leu Gly 115 120 Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly Pro Arg Arg 135 Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg Glu Ala Gly 145 Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Gly Gly Ser 165 170 Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg Gly Ala Ala

DID

Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp Ala His Pro

Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val Val Ser Pro

1716

Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala Leu Ser Gly 235 Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His Ala Gly Pro 250 Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro Cys Pro Pro 260 Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly Asp Lys Glu 280 Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser Arg Pro Trp 310 Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln Arg Tyr Trp 330 Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg Ala Ala Val 360 Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu Val Gln Leu 385 395 Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser Arg His Asn 425 Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met Ser Val Arg 455 Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe Leu His Trp 490 Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe Phe Tyr Val 500 Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr Arg Lys Ser 520 525

Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His Leu Lys Arg 530 535 Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln His Arg Glu 555 Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile Pro Lys Pro 570 Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser Arg Val Lys 600 Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg Ala Trp Arg 630 Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Glu Leu Tyr 650 Phe Val Lys Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro 665 Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala 680 His Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu Thr Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu Thr 705 Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Leu Asn Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys His 745 His Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly Ile Pro Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly 775 Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu 790 Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His 805 810

Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly

825

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Cys Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp
                             840
 Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly Leu
 Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val Gln
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 Ser Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu Thr
                 885
                                     890
Phe Asn Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu Phe
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Gly Val Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln Val
                             920
Asn Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu Leu
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Gln Ala Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe His Gln
Gln Val Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp Thr
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Ala Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala Gly Met Ser
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Trp Leu Cys His Gln Ala Phe Leu Leu Lys Leu Thr Arg His Arg Val
Thr Tyr Val Pro Leu Leu Gly Ser Leu Arg Thr Ala Gln Thr Gln Leu
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NO:75 with Intron Y ORF3

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DIO

305

320

Ser Trp Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe

Cys Val Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu

295

Gly Ala Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln 330 His His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp 345 Thr Pro Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu 375 Arg Pro Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu 390 400 Gly Ser Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu 410 Pro Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly 425 Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro 440 Leu Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys 450 Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg 470 475 Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe 520 Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp 535 Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val 550 555 Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala 565 Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg 585 Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe

DID

Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg

Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val

940

Phe Pro Val Glu Asp Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Met

935

Pro Ala His Gly Leu Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg 945 Thr Leu Glu Val Gln Ser Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile 970 Arg Ala Ser Leu Thr Phe Asn Arg Gly Phe Lys Ala Gly Arg Asn Met 985 Arg Arg Lys Leu Phe Gly Val Leu Arg Leu Lys Cys His Ser Leu Phe 995 1000 Leu Asp Leu Gln Val Asn Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr 1015 Lys Ile Leu Leu Gln Ala Tyr Arg Phe His Ala Cys Val Leu Gln 1025 1030 1040 Leu Pro Phe His Gln Gln Val Trp Lys Asn Pro Thr Phe Phe Leu Arg 1045 Val Ile Ser Asp Thr Ala Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys 1060 1065 Asn Ala Gly Met Ser Leu Gly Ala Lys Gly Ala Ala Gly Pro Leu Pro 1080 Ser Glu Ala Val Gln Trp Leu Cys His Gln Ala Phe Leu Leu Lys Leu 1090 1095 Thr Arg His Arg Val Thr Tyr Val Pro Leu Leu Gly Ser Leu Arg Thr

1105 1110 1115 Ser Leu Arg Thr 1105 1120

Ala Gln Thr Gln Leu Ser Arg Lys Leu Pro Gly Thr Thr Leu Thr Ala 1125 1130 1135

Leu Glu Ala Ala Ala Asn Pro Ala Leu Pro Ser Asp Phe Lys Thr Ile 1140 1145 1150

Leu Asp

20

<210> 79 <211> 3137 <212> DNA <213> Homo sapiens <220>

<223> Truncated Protein Lacking Motif A (ver.2); with Introns Y, Beta and 2

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cgcggggacc cggcggcttt ccgcgcgctg gtggcccagt gcctggtgtg cgtgccctgg 180
gacgcacggc cgccccccc cgcccctcc ttccgccagg tgggcctcc cgggggtcggc 240

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 gggcccgcgg gggccccccc gaggccttca ccaccagcgt gcgcagctac ctgcccaaca 480
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 ccccgccaca cgctagtgga ccccgaaggc gtctgggatg cgaacgggcc tggaaccata 720
 gcgtcaggga ggccggggtc cccctgggcc tgccagcccc gggtgcgagg aggcgcgggg 780
 gcagtgccag ccgaagtctg ccgttgccca agaggcccag gcgtggcgct gcccctgagc 840
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ctgtgctatt ttggtaa
                                                                 3137
<210> 80
<211> 970
<212> PRT
<213> Homo sapiens
<220>
<223> Truncated Protein lacking Motif A (ver.2); encoded
     by SEQ ID NO:79 with Intron Y ORF1
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131

DIO

<400> 80 Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly 25 Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Gly Leu Pro Gly Val Gly Val Arg Leu Gly Leu Arg Ala Ala Gly Gly Asn Gln Arg His Ala Glu Ser Ser Ala Gly Asp Ser Gly Arg Phe Pro Arg Arg Ser Cys Leu Lys Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys 120 Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly 130 135 Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr 150 Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg 170 Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser 230 Val Arg Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro 265 Arg Arg Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly

Ser Trp Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe

295

Cys Val Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu 305 Gly Ala Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln 330 His His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp 345 Thr Pro Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu 375 Arg Pro Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu 400 Gly Ser Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu 410 Pro Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys 450 Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr 490 Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe 520 Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp 535 Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val 550 Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala 565 Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg 585 Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe

595

Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg 615 Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val 630 635 Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg 650 Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala 695 Arg Arg Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile 720 His Arg Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro 730 Pro Pro Glu Leu Tyr Phe Val Lys Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu Thr Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu Thr Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln 810 Ser Ser Ser Leu Asn Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys His His Ala Val Arg Ile Arg Gly Lys Ser Tyr Val 840 Gln Cys Gln Gly Ile Pro Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg 870 Arg Asp Gly Leu Leu Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr 885 Pro His Leu Thr His Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly 905 Val Pro Glu Tyr Gly Cys Val Val Asn Leu Arg Lys Thr Val Val Asn

Phe Pro Val Glu Asp Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Met 930 935 940

Pro Ala His Gly Leu Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg 945 950 955 960

Thr Leu Glu Val Gln Ser Asp Tyr Ser Arg 965 970

<210> 81

<211> 885

<212> PRT

<213> Homo sapiens

<220>

<223> Truncated Protein lacking Motif A (ver.2); encoded by SEQ ID NO:79 with Intron Y ORF2 after the termination codon

<400> 81

Gly Arg Pro Gly Gly Thr Ser Asp Met Arg Arg Ala Ala Gln Ala Thr
1 5 10 15

Gln Gly Ala Ser Pro Ala Gly Ser Cys Leu Lys Glu Leu Val Ala Arg
20 25 30

Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val Leu Ala Phe 35 40 45

Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro Glu Ala Phe 50 55 60

Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr Asp Ala Leu 65 70 75 80

Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val Gly Asp Asp 85 90 95

Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val Leu Val Ala 100 105 110

Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr Gln Leu Gly
115 120 125

Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly Pro Arg Arg 130 135 140

Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg Glu Ala Gly
145 150 155 160

Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Gly Gly Ser 165 170 175

Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg Gly Ala Ala 180 185 190

Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val Val Ser Pro 215 Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala Leu Ser Gly 230 Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His Ala Gly Pro 245 Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro Cys Pro Pro 265 Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser Arg Pro Trp 310 315 Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln Arg Tyr Trp 325 330 Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His Ala Gln Cys 340 Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln Gly Ser Val 375 Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu Val Gln Leu 385 Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe Val Arg Ala 410 Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser Arg His Asn 420 425 Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser Leu Gly Lys 440 His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met Ser Val Arg 450 Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys Val Pro Ala 470 475 Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe Leu His Trp 490

D/0

Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr Arg Lys Ser 520 Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His Leu Lys Arg 535 Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln His Arg Glu 550 Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile Pro Lys Pro 570 Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val Gly Ala Arg 585 Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg Ala Trp Arg 630 635 Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro Glu Leu Tyr Phe Val Lys Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro 660 Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala 680 His Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu Thr Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu Thr Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu Asn 730 Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys His 740 His Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly Ile Pro Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly 770 Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu 795 Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His

D/0

Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly 820 825 830

Cys Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp 835 840 845

Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly Leu 850 855 860

Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val Gln 865 870 875

Ser Asp Tyr Ser Arg 885

<210> 82

<211> 970

<212> PRT

<213> Homo sapiens

<220>

1010

<223> Truncated Protein lacking Motif A (ver.2); encoded
by SEQ ID NO:79 with Intron Y ORF3

<400> 82

Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser 1 5 10 15

His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
20 25 30

Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg 35 40 45

Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro 50 60

Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Pro Pro Arg Gly Arg Arg 65 70 75 80

Pro Ala Gly Val Glu Gly Gly Arg Gly Glu Pro Ala Thr Cys Gly Glu 85 90 95

Gln Arg Arg Leu Arg Ala Leu Pro Pro Gln Val Ser Cys Leu Lys 100 105 110

Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys
115 120 125

Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly 130 135 140

Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr 145 150 155 160

Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg 170 Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu 185 Phe Val Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro 200 Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg 250 Arg Arg Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly 280 Ser Trp Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe 290 295 Cys Val Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu 305 Gly Ala Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln 330 His His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu 380 Arg Pro Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu 390 395 Gly Ser Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu 405 Pro Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly 425 Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg

465					470					475					480
Arg	Leu	Val	Gln	Leu 485	Leu	Arg	Gln	His	Ser 490	Ser	Pro	Trp	Gln	Val 495	Tyr
Gly	Phe	Val	Arg 500	Ala	Cys	Leu	Arg	Arg 505	Leu	Val	Pro	Pro	Gly 510	Leu	Trp
Gly	Ser	Arg 515	His	Asn	Glu	Arg	Arg 520	Phe	Leu	Arg	Asn	Thr 525		Lys	Phe
Ile	Ser 530	Leu	Gly	Lys	His	Ala 535	Lys	Leu	Ser	Leu	Gln 540	Glu	Leu	Thr	Trp
Lys 545	Met	Ser	Val	Arg	Asp 550	Cys	Ala	Trp	Leu	Arg 555	Arg	Ser	Pro	Gly	Val 560
Gly	Cys	Val	Pro	Ala 565	Ala	Glu	His	Arg	Leu 570	Arg	Glu	Glu	Ile	Leu 575	Ala
Lys	Phe	Leu	His 580	Trp	Leu	Met	Ser	Val 585	Tyr	Val	Val	Glu	Leu 590	Leu	Arg
Ser	Phe	Phe 595	Tyr	Val	Thr	Glu	Thr 600	Thr	Phe	Gln	Lys	Asn 605	Arg	Leu	Phe
Phe	Tyr 610	Arg	Lys	Ser	Val	Trp 615	Ser	Lys	Leu	Gln	Ser 620	Ile	Gly	Ile	Arg
Gln 625	His	Leu	Lys	Arg	Val 630	Gln	Leu	Arg	Glu	Leu 635	Ser	Glu	Ala	Glu	Val 640
Arg	Gln	His	Arg	Glu 645	Ala	Arg	Pro	Ala	Leu 650	Leu	Thr	Ser	Arg	Leu 655	Arg
Phe	Ile	Pro	Lys 660	Pro	Asp	Gly	Leu	Arg 665	Pro	Ile	Val	Asn	Met 670	Asp	Tyr
Val	Val	Gly 675	Ala	Arg	Thr	Phe	Arg 680	Arg	Glu	Lys	Arg	Ala 685	Glu	Arg	Leu
Thr	Ser 690	Arg	Val	Lys	Ala	Leu 695	Phe	Ser	Val	Leu	Asn 700	Tyr	Glu	Arg	Ala
Arg 705	Arg	Pro	Gly	Leu	Leu 710	Gly	Ala	Ser	Val	Leu 715	Gly	Leu	Asp	Asp	Ile 720

Ser Ile Ile Lys Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His Gly His Val Arg Lys Ala Phe Lys Ser His

His Arg Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro

Pro Pro Glu Leu Tyr Phe Val Lys Asp Arg Leu Thr Glu Val Ile Ala

Val Ser Thr Leu Thr Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala 785 His Leu Gln Glu Thr Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln 810 Ser Ser Ser Leu Asn Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys His His Ala Val Arg Ile Arg Gly Lys Ser Tyr Val 835 840 Gln Cys Gln Gly Ile Pro Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys 855 Ser Leu Cys Tyr Gly Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg 870 880 Arg Asp Gly Leu Leu Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr 890 Pro His Leu Thr His Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly 900 905 Val Pro Glu Tyr Gly Cys Val Val Asn Leu Arg Lys Thr Val Val Asn 920 Phe Pro Val Glu Asp Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Met 930 Pro Ala His Gly Leu Phe Pro Trp Cys Gly Leu Leu Asp Thr Arg 945 955 Thr Leu Glu Val Gln Ser Asp Tyr Ser Arg <210> 83 <211> 3432 <212> DNA <213> Homo sapiens <220> <223> Protein Lacking Motif A and Altered C-Terminus (ver.2); with Intron Y, Beta and 3 <400> 83 atgccgcgcg ctccccgctg ccgagccgtg cgctccctgc tgcgcagcca ctaccgcgag 60 gtgctgccgc tggccacgtt cgtgcggcgc ctggggcccc agggctggcg gctggtgcag 120 cgcggggacc cggcggcttt ccgcgcgctg gtggcccagt gcctggtgtg cgtgcctgg 180 gacgcacggc cgcccccgc cgccccctcc ttccgccagg tgggcctccc cggggtcggc 240 gtccggctgg ggttgagggc ggccgggggg aaccagcgac atgcggagag cagcgcaggc 300 gactcagggc gcttcccccg caggtgtcct gcctgaagga gctggtggcc cgagtgctgc 360 agaggetgtg egagegegge gegaagaaeg tgetggeett eggettegeg etgetggaeg 420

gggcccgcgg gggcccccc gaggccttca ccaccagcgt gcgcagctac ctgcccaaca 480 cggtgaccga cgcactgcgg gggagcgggg cgtgggggct gctgctgcgc cgcgtgggcg 540 acgacgtgct ggttcacctg ctggcacgct gcgcgctctt tgtgctggtg gctcccagct 600

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<210> 84
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<213> Homo sapiens
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      (ver.2); encoded by SEQ ID NO:83 with Intron Y
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D10

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Pro	Glr	1 Gly 39	y Trp	Arg	J Leu	Val	Gln 40		gly	Asp) Pro	Ala 45		a Phe	e Arg
Ala	Let 50	ı Val	l Ala	a Glr	Cys	Leu 55	Val	Cys	Val	Pro	Trp 60		Ala	a Arg	J Pro
Pro 65	Pro	Ala	a Ala	Pro	Ser 70	Phe	Arg	Gln	Val	Gly 75		Pro	Gly	⁄ Val	Gly 80
Val	Arg	l Leu	ı Gly	Leu 85	Arg	Ala	Ala	Gly	Gly 90		Gln	Arg	His	Ala 95	Glu
Ser	Ser	Ala	Gly 100	Asp	Ser	Gly	Arg	Phe 105	Pro	Arg	Arg	Ser	Cys 110		Lys
Glu	Leu	Val 115	Ala	Arg	Val	Leu	Gln 120	Arg	Leu	Cys	Glu	Arg 125	Gly	Ala	Lys
Asn	Val 130	Leu	Ala	Phe	Gly	Phe 135	Ala	Leu	Leu	Asp	Gly 140	Ala	Arg	Gly	Gly
Pro 145	Pro	Glu	Ala	Phe	Thr 150	Thr	Ser	Val	Arg	Ser 155	Tyr	Leu	Pro	Asn	Thr 160
Val	Thr	Asp	Ala	Leu 165	Arg	Gly	Ser	Gly	Ala 170	Trp	Gly	Leu	Leu	Leu 175	Arg
Arg	Val	Gly	Asp 180	Asp	Val	Leu	Val	His 185	Leu	Leu	Ala	Arg	Cys 190	Ala	Leu
Phe	Val	Leu 195	Val	Ala	Pro	Ser	Cys 200	Ala	Tyr	Gln	Val	Cys 205	Gly	Pro	Pro
Leu	Tyr 210	Gln	Leu	Gly	Ala	Ala 215	Thr	Gln	Ala	Arg	Pro 220	Pro	Pro	His	Ala
Ser 225	Gly	Pro	Arg	Arg	Arg 230	Leu	Gly	Cys	Glu	Arg 235	Ala	Trp	Asn	His	Ser 240
Val	Arg	Glu	Ala	Gly 245	Val	Pro	Leu	Gly	Leu 250	Pro	Ala	Pro	Gly	Ala 255	Arg
Arg	Arg	Gly	Gly 260	Ser	Ala	Ser	Arg	Ser 265	Leu	Pro	Leu	Pro	Lys 270	Arg	Pro
Arg	Arg	Gly 275	Ala	Ala	Pro	Glu	Pro 280	Glu	Arg	Thr		Val 285	Gly	Gln	Gly
Ser	Trp 290	Ala	His	Pro	Gly .	Arg 295	Thr .	Arg	Gly		Ser . 300	Asp	Arg	Gly	Phe

D/0

Cys Val Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu 305 Gly Ala Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln 325 330 His His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp 345 Thr Pro Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser 360 Ser Gly Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu 375 Arg Pro Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu 400 Gly Ser Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu 410 Pro Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly 420 425 Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys 450 Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg 475 Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr 490 Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe 520 Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp 530 535 Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val 550 Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala 565 Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg 585 Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe 600

Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val 630 635 Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg 645 650 Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala 695 Arg Arg Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro 730 Pro Pro Glu Leu Tyr Phe Val Lys Asp Arg Leu Thr Glu Val Ile Ala 745 Ser Ile Ile Lys Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His Gly His Val Arg Lys Ala Phe Lys Ser His 770 Val Ser Thr Leu Thr Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala 790 His Leu Gln Glu Thr Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu Asn Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys His His Ala Val Arg Ile Arg Gly Lys Ser Tyr Val 840 Gln Cys Gln Gly Ile Pro Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys 850 Ser Leu Cys Tyr Gly Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg 870 875 Arg Asp Gly Leu Leu Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly 905

Val Pro Glu Tyr Gly Cys Val Val Asn Leu Arg Lys Thr Val Val Asn

915

920

925

Phe Pro Val Glu Asp Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Met 930 940

Pro Ala His Gly Leu Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg 945 950 955 960

Thr Leu Glu Val Gln Ser Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile 965 970 975

Arg Ala Ser Leu Thr Phe Asn Arg Gly Phe Lys Ala Gly Arg Asn Met 980 985 990

Arg Arg Lys Leu Phe Gly Val Leu Arg Leu Lys Cys His Ser Leu Phe 995 1000 1005

Leu Asp Leu Gln Val Asn Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr 1010 1015 1020

Lys Ile Leu Leu Gln Ala Tyr Arg Phe His Ala Cys Val Leu Gln 1025 1030 1035 1040

Leu Pro Phe His Gln Gln Val Trp Lys Asn Pro Thr Phe Phe Leu Arg
1045 1050 1055

Val Ile Ser Asp Thr Ala Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys 1060 1065 1070

Asn Ala Glu Glu Asn Ile Leu Val Val Thr Pro Ala Val Leu Gly 1075 1080 1085

Ser Gly Gln Pro Glu Met Glu Pro Pro Arg Arg Pro Ser Gly Val Gly 1090 1095 1100

Ser Phe Pro Val Ser Pro Gly Arg Gly Val Gly Leu Gly Leu Phe Ile 1105 1110 1115 1120

Gly Ala

D10

<210> 85

<211> 1037

<212> PRT

<213> Homo sapiens

<220>

<223> Protein Lacking Motif A and Altered C-Terminus
 (ver.2); encoded by SEQ ID NO:83 with Intron Y
 ORF2 after the termination codon

<400> 85

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Gln Gly Ala Ser Pro Ala Gly Ser Cys Leu Lys Glu Leu Val Ala Arg 20 25 30

Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr Asp Ala Leu 70 Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val Leu Val Ala 105 Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg Glu Ala Gly 150 155 Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Gly Gly Ser 170 Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg Gly Ala Ala 180 Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala Leu Ser Gly 230 240 Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His Ala Gly Pro 250 Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro Cys Pro Pro 260 265 Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly Asp Lys Glu 280 Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro Ser Leu Thr 290 Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser Arg Pro Trp 310 315 Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln Arg Tyr Trp 330

DID

Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg Ala Ala Val 360 Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln Gly Ser Val 375 Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu Val Gln Leu 390 Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe Val Arg Ala 410 Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser Arg His Asn 425 Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser Leu Gly Lys 435 His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys Val Pro Ala 470 475 Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe Phe Tyr Val 500 Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln His Arg Glu 545 550 Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile Pro Lys Pro 570 Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val Gly Ala Arg 585 Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser Arg Val Lys 600 Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Pro Gly Leu 610 Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg Ala Trp Arg 635 Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Glu Leu Tyr

Ph€	e Val	. Lys	Asp 660	Arg	g Leu	ı Thr	Glu	Val		e Ala	Ser	Ile	: Ile 670		Pro
Glr	a Asr	1 Thr 675		Cys	val	Arg	Arg 680		Ala	val	Val	Gln 685		Ala	Ala
His	Gly 690	His	Val	Arc	i ràs	Ala 695		Lys	Ser	His	Val 700		Thr	Leu	Thr
Asp 705	Leu	Glr	Pro	Tyr	Met 710		Gln	Phe	· Val	Ala 715		Leu	Gln	Glu	Thr 720
Ser	Pro	Leu	Arg	Asp 725	Ala	Val	Val	Ile	Glu 730		Ser	Ser	Ser	Leu 735	Asn
Glu	Ala	Ser	Ser 740	Gly	Leu	Phe	Asp	Val 745		Leu	Arg	Phe	Met 750	Cys	His
His	Ala	Val 755	Arg	Ile	Arg	Gly	Lys 760	Ser	Tyr	Val	Gln	Cys 765	Gln	Gly	Ile
Pro	Gln 770	Gly	Ser	Ile	Leu	Ser 775	Thr	Leu	Leu	Cys	Ser 780	Leu	Cys	Tyr	Gly
Asp 785	Met	Glu	Asn	Lys	Leu 790	Phe	Ala	Gly	Ile	Arg 795	Arg	Asp	Gly	Leu	Leu 800
Leu	Arg	Leu	Val	Asp 805	Asp	Phe	Leu	Leu	Val 810	Thr	Pro	His	Leu	Thr 815	His
Ala	Lys	Thr	Phe 820	Leu	Arg	Thr	Leu	Val 825	Arg	Gly	Val	Pro	Glu 830	Tyr	Gly
Cys	Val	Val 835	Asn	Leu	Arg	Lys	Thr 840	Val	Val	Asn	Phe	Pro 845	Val	Glu	Asp
Glu	Ala 850	Leu	Gly	Gly	Thr	Ala 855	Phe	Val	Gln	Met	Pro 860	Ala	His	Gly	Leu
Phe 865	Pro	Trp	Cys	Gly	Leu 870	Leu	Leu	Asp		Arg 875	Thr	Leu	Glu	Val	Gln 880
Ser	Asp	Tyr	Ser	Ser 885	Tyr	Ala	Arg	Thr	Ser 890	Ile	Arg	Ala	Ser	Leu 895	Thr
Phe	Asn	Arg	Gly 900	Phe	Lys	Ala	Gly	Arg 905	Asn	Met	Arg	Arg	Lys 910	Leu	Phe
Gly	Val	Leu 915	Arg	Leu	Lys	Cys	His 920	Ser	Leu	Phe	Leu	Asp 925	Leu	Gln	Val
Asn	Ser 930	Leu	Gln	Thr	Val	Cys 935	Thr	Asn	Ile	Tyr	Lys 940	Ile	Leu	Leu	Leu
Gln 945	Ala	Tyr	Arg	Phe	His 950	Ala	Cys	Val	Leu	Gln 955	Leu	Pro	Phe		Gln 960

Asn Ile Leu Val Val Thr Pro Ala Val Leu Gly Ser Gly Gln Pro Glu 995 1000 1005

Met Glu Pro Pro Arg Arg Pro Ser Gly Val Gly Ser Phe Pro Val Ser 1010 1015 1020

Pro Gly Arg Gly Val Gly Leu Gly Leu Phe Ile Gly Ala 1025 1030 1035

<210> 86

<211> 1122

<212> PRT

<213> Homo sapiens

<220>

<223> Protein Lacking Motif A and Altered C-Terminus
 (ver.2); encoded by SEQ ID NO:83 with Intron Y
 ORF3

<400> 86

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His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
20 25 30

Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
35 40 45

Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro 50 60

Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Pro Pro Arg Gly Arg Arg 65 70 75 80

Pro Ala Gly Val Glu Gly Gly Arg Gly Glu Pro Ala Thr Cys Gly Glu 85 90 95

Gln Arg Arg Leu Arg Ala Leu Pro Pro Gln Val Ser Cys Leu Lys 100 105 110

Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys
115 120 125

Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly 130 135 140

Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr 145 150 155 160

Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg 170 Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro 200 Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala 215 Ser Gly Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg 250 Arg Arg Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln 325 His His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser 360 Ser Gly Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu 390 395 Gly Ser Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu 405 410 Pro Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly 425 Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro 435 Leu Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys 455

Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg

151

DIS

465					470					475					480
Arg	Leu	Val	Gln	Leu 485		Arg	Gln	His	Ser 490		Pro	Trp	Gln	Val 495	Tyr
Gly	Phe	Val	Arg 500	Ala	Cys	Leu	Arg	Arg 505	Leu	Val	Pro	Pro	Gly 510	Leu	Trp
Gly	Ser	Arg 515	His	Asn	Glu	Arg	Arg 520	Phe	Leu	Arg	Asn	Thr 525	Lys	Lys	Phe
Ile	Ser 530	Leu	Gly	Lys	His	Ala 535	Lys	Leu	Ser	Leu	Gln 540	Glu	Leu	Thr	Trp
Lys 545	Met	Ser	Val	Arg	Asp 550	Cys	Ala	Trp	Leu	Arg 555	Arg	Ser	Pro	Gly	Val 560
Gly	Cys	Val	Pro	Ala 565	Ala	Glu	His	Arg	Leu 570	Arg	Glu	Glu	Ile	Leu 575	Ala
Lys	Phe	Leu	His 580	Trp	Leu	Met	Ser	Val 585	Tyr	Val	Val	Glu	Leu 590	Leu	Arg
Ser	Phe	Phe 595	Tyr	Val	Thr	Glu	Thr 600	Thr	Phe	Gln	Lys	Asn 605	Arg	Leu	Phe
Phe	Tyr 610	Arg	Lys	Ser	Val	Trp 615	Ser	Lys	Leu	Gln	Ser 620	Ile	Gly	Ile	Arg
Gln 625	His	Leu	Lys	Arg	Val 630	Gln	Leu	Arg	Glu	Leu 635	Ser	Glu	Ala	Glu	Val 640
Arg	Gln	His	Arg	Glu 645	Ala	Arg	Pro	Ala	Leu 650	Leu	Thr	Ser	Arg	Leu 655	Arg
Phe	Ile	Pro	Lys 660	Pro	Asp	Gly	Leu	Arg 665	Pro	Ile	Val	Asn	Met 670	Asp	Tyr
Val	Val	Gly 675	Ala	Arg	Thr	Phe	Arg 680	Arg	Glu	Lys	Arg	Ala 685	Glu	Arg	Leu
Thr	Ser 690	Arg	Val	Lys	Ala	Leu 695	Phe	Ser	Val	Leu	Asn 700	Tyr	Glu	Arg	Ala
Arg 705	Arg	Pro	Gly	Leu	Leu 710	Gly	Ala	Ser	Val	Leu 715	Gly	Leu	Asp	Asp	Ile 720
His	Arg	Ala	Trp	Arg 725	Thr	Phe	Val	Leu	Arg 730	Val	Arg	Ala	Gln	Asp 735	Pro
Pro	Pro	Glu	Leu 740	Tyr	Phe	Val	Lys	Asp 745	Arg	Leu	Thr	Glu	Val 750	Ile	Ala
Ser	Ile	Ile 755	Lys	Pro	Gln	Asn	Thr 760	Tyr	Cys	Val	Arg	Arg 765	Tyr	Ala	Val
Val	Gln 770	Lys	Ala	Ala	His	Gly 775	His	Val	Arg	Lys	Ala 780	Phe	Lys	Ser	His

Val Ser Thr Leu Thr Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu Thr Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln 805 810 Ser Ser Ser Leu Asn Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu 820 Arg Phe Met Cys His His Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly Ile Pro Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys 855 Ser Leu Cys Tyr Gly Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg 870 Arg Asp Gly Leu Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr 890 Pro His Leu Thr His Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly 900 Val Pro Glu Tyr Gly Cys Val Val Asn Leu Arg Lys Thr Val Val Asn 920 Phe Pro Val Glu Asp Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Met 930 Pro Ala His Gly Leu Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val Gln Ser Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile 970 Arg Ala Ser Leu Thr Phe Asn Arg Gly Phe Lys Ala Gly Arg Asn Met 980 Arg Arg Lys Leu Phe Gly Val Leu Arg Leu Lys Cys His Ser Leu Phe 1000 Leu Asp Leu Gln Val Asn Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr 1010 1015 Lys Ile Leu Leu Gln Ala Tyr Arg Phe His Ala Cys Val Leu Gln 1030 1035 Leu Pro Phe His Gln Gln Val Trp Lys Asn Pro Thr Phe Phe Leu Arg 1045 Val Ile Ser Asp Thr Ala Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys 1065 Asn Ala Glu Glu Asn Ile Leu Val Val Thr Pro Ala Val Leu Gly 1075 1080

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gatgtcgctg ggggccaagg gcgccgccgg ccctctgccc tccgaggccg tgcagtggct 7500
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<220>
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<223> Wherein Xaa is any residue
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Gly
<210> 93
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<220>
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Pro Xaa Xaa Xaa Pro Xaa Xaa Pro
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His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr
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                                      10
Pro
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<223> Wherein N is G, U, C or A
<220>
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<221> modified base

<222>	· ·	
	Wherein N is G, U, C or A	
<220><221>	modified base	
<222>	(9)(14)	
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<423>	Primer Design Based on EST Sequence	
	Accession Number AA281296	
<400>	97	
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(213)	metricial boquesos	
<220>	Demonistra of Autificial Company	Amplification
<223>	Description of Artificial Sequence: Primer Design Based on EST Sequence	
	Accession Number AA281296	
<400>	98	
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Accession Number AA281296

<400>	99 cttg aattcacatc tcaccatgaa ggagctggtg gcccgagt	48
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Amplification Primer Design based on EST Sequence GenBank Accession Number AA281296

<400> 108 cactggctga tgagtgtgta c	21
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<210> 111 <211> 20 <212> DNA <213> Artificial Sequence	
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<210><211><212>	121 21	22
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gaggtgcaga gcgactactc ca	22
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<210> 133 <211> 19 <212> DNA <213> Artificial Sequence	
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<210><211><211><212><213>	24	
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<400> gcagca	139 caca tgcgtgaaac ctgt	24
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	GenBank Accession Number AA281296	EST Sequence	
	Genbank Accession Number AA201290		
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-	gagte etg	, cragooggeg megemegege	73
, ,	, 3		
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	Amplification Primer Design based on	EST Sequence	
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400	145		
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0.1.0	***		
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Amplification Primer Design based on EST Sequence GenBank Accession Number AA281296

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      Amplification Primer Design based on EST Sequence
      GenBank Accession Number AA281296
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Val Gln Met Pro Ala His
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Val Gly Leu Gly Leu
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<211> 4
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Arg Ala Thr Ser
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<211> 622
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      by SEQ ID NO:51, with Y Intron ORF3
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His Thr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
             20
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Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Pro Pro Arg Gly Arg Arg
Pro Ala Gly Val Glu Gly Gly Arg Gly Glu Pro Ala Thr Cys Gly Glu
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Gln Arg Arg Leu Arg Ala Leu Pro Pro Gln Val Ser Cys Leu Lys
            100
                                105
                                                    110
Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys
                            120
Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly
    130
                        135
Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr
                    150
                                        155
Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Arg
Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu
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Phe Val Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro

		1))					200					200			
Leu	Tyr 210	Gln	Leu	Gly	Ala	Ala 215	Thr	Gln	Ala	Arg	Pro 220	Pro	Pro	His	Ala
Ser 225	Gly	Pro	Arg	Arg	Arg 230	Leu	Gly	Cys	Glu	Arg 235	Ala	Trp	Asn	His	Ser 240
Val	Arg	Glu	Ala	Gly 245	Val	Pro	Leu	Gly	Leu 250	Pro	Ala	Pro	Gly	Ala 255	Arg
Arg	Arg	Gly	Gly 260	Ser	Ala	Ser	Arg	Ser 265	Leu	Pro	Leu	Pro	Lys 270	Arg	Pro
Arg	Arg	Gly 275	Ala	Ala	Pro	Glu	Pro 280	Glu	Arg	Thr	Pro	Val 285	Gly	Gln	Gly
Ser	Trp 290	Ala	His	Pro	Gly	Arg 295	Thr	Arg	Gly	Pro	Ser 300	Asp	Arg	Gly	Phe
Cys 305	Val	Val	Ser	Pro	Ala 310	Arg	Pro	Ala	Glu	Glu 315	Ala	Thr	Ser	Leu	Glu 320
Gly	Ala	Leu	Ser	Gly 325	Thr	Arg	His	Ser	His 330	Pro	Ser	Val	Gly	Arg 335	Gln
His	His	Ala	Gly 340	Pro	Pro	Ser	Thr	Ser 345	Arg	Pro	Pro	Arg	Pro 350	Trp	Asp
Thr	Pro	Cys 355	Pro	Pro	Val	Tyr	Ala 360	Glu	Thr	Lys	His	Phe 365	Leu	Tyr	Ser
Ser	Gly 370	Asp	Lys	Glu	Gln	Leu 375	Arg	Pro	Ser	Phe	Leu 380	Leu	Ser	Ser	Leu
Arg 385	Pro	Ser	Leu	Thr	Gly 390	Ala	Arg	Arg	Leu	Val 395	Glu	Thr	Ile	Phe	Leu 400
Gly	Ser	Arg	Pro	Trp 405	Met	Pro	Gly	Thr	Pro 410	Arg	Arg	Leu	Pro	Arg 415	Leu
Pro	Gln	Arg	Tyr 420	Trp	Gln	Met	Arg	Pro 425	Leu	Phe	Leu	Glu	Leu 430	Leu	Gly
Asn	His	Ala 435	Gln	Cys	Pro	Tyr	Gly 440	Val	Leu	Leu	Lys	Thr 445	His	Cys	Pro
Leu	Arg 450	Ala	Ala	Val	Thr	Pro 455	Ala	Ala	Gly	Val	Cys 460	Ala	Arg	Glu	Lys
Pro 465	Gln	Gly	Ser	Val	Ala 470	Ala	Pro	Glu	Glu	Glu 475	Asp	Thr	Asp	Pro	Arg 480
Arg	Leu	Val	Gln	Leu 485	Leu	Arg	Gln	His	Ser 490	Ser	Pro	Trp	Gln	Val 495	Tyr
Gly	Phe	Val	Arg		Cys	Leu	Arg	Arg 505		Val	Pro	Pro	Gly 510		Trp

Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe 515

Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp 530

Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val 545

Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala 565

Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Arg S90

Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe 595

Phe Tyr Arg Lys Ser Val Trp 615

Ser Lys Leu Gln Ser Ile Gly